

4 protein - protein search, using sw model		Search time 15.21 Seconds (without alignments) 20.233 Million cell updates/sec		
Run on: November 14, 2000, 11:54:42 ;		Search time 15.21 Seconds (without alignments) 20.233 Million cell updates/sec		
Scoring table:	BLOSUM62	Maxgap 10.0 , Gapext 0.5		
Scanned:	268485 seqs.	34193795 residues		
Total number of hits satisfying chosen parameters:	268485			
Minimum DB seq length:	0			
Maximum DB seq length:	2000000000			
Cost-processing: Minimum Match 0%				
Maximum Match 100%				
Listing first 45 summaries				
Database:	A_Geneseq_36 *			
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	6:	/SIDS1/seqdata/geneseq/geneseqp/AA1985.DAT:*		
	7:	/SIDS1/seqdata/geneseq/geneseqp/AA1986.DAT:*		
	8:	/SIDS1/seqdata/geneseq/geneseqp/AA1987.DAT:*		
	9:	/SIDS1/seqdata/geneseq/geneseqp/AA1989.DAT:*		
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	13:	/SIDS1/seqdata/geneseq/geneseqp/AA1993.DAT:*		
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	20:	/SIDS1/seqdata/geneseq/geneseqp/AA2000.DAT:*		
	21:	/SIDS1/seqdata/geneseq/geneseqp/AA2001.DAT:*		
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES				
8				
result no.	Score	Query Match Length	DB ID	Description
1	43	100.0	9	15 R73685 Antigen fragment 1
2	43	100.0	9	17 R97507 Cytotoxic T lympho
3	43	100.0	9	18 W36824 Immunogenic peptid
4	43	100.0	9	19 W77131 HER-2/neu syntheti
5	43	100.0	9	19 W78859 HER-1/he protein
6	43	100.0	9	19 W70057 HER-2/neu derived
7	43	100.0	9	20 Y10495 HLA Class I motif
8	43	100.0	15	21 Y98846 HLA class II bind
9	43	100.0	624	11 R08222 Extracellular domain
10	43	100.0	782	18 W19764 Her2-GM-CSF immuno
11	43	100.0	951	21 W01111 DC8sacrv-erbB2EC fu
12	43	100.0	1255	17 W01111 Her2-2/neu protein

13	43	100.0	1255	20	W92406
14	43	100.0	1255	21	YB#780
15	43	100.0	1255	21	Y93630
16	40	93.0	1433	14	R3968
17	32	74.4	932	19	WB#040
18	32	74.4	933	19	WB#039
19	31	72.4	128	17	P60883
20	31	72.1	205	21	Y73298
21	31	72.1	219	20	Y34701
22	31	72.1	686	15	R60336
23	31	72.1	687	20	Y13937
24	30	69.8	195	18	W00922
25	30	69.8	269	15	R48743
26	30	69.8	269	17	W02715
27	30	69.8	283	21	Y93353
28	30	69.8	790	17	R93565
29	30	69.8	790	17	R93568
30	30	69.8	791	17	R93566
31	30	69.8	792	17	R93567
32	29	67.4	17	21	Y86381
33	29	67.4	24	16	R63280
34	29	67.4	41	19	W75141
35	29	67.4	42	19	W75076
36	29	67.4	58	20	W67890
37	29	67.4	127	18	W36348
38	29	67.4	132	21	Y86313
39	29	67.4	133	20	W67911
40	29	67.4	144	19	W98463
41	29	67.4	186	20	W89879
42	29	67.4	296	20	Y39859
43	29	67.4	332	18	W20914
44	29	67.4	443	21	Y86230
45	29	67.4	457	9	P80299
					ALIGNMENTS
					RESULT
					1
					R73685 standard; peptide: 9 AA.
					ID
					XX
					AC
					R73685;
					XX
					DT
					14-JUN-1995 (first entry)
					XX
					DE
					Antigen fragment 1, from c-ERBB2 has binding affinity for HLA-2.1.
					XX
					KW
					antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV;
					KW
					HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;
					KW
					human immunodeficiency virus; human papilloma virus; PS3; c-ERBB2;
					KW
					MaCE-1; melanoma antigen-1; core antigen; surface antigen;
					KW
					pharmaceutical composition; in vivo; ex vivo; therapeutic;
					KW
					diagnostic; MHC class I molecule; major histocompatibility complex;
					KW
					HLA-A2.1; 9mer; 1omer; anchor; human leukocyte antigen; PLP; 8mer;
					KW
					algorithm prediction; NBP; CMV; cytomegalovirus; HSV;
					KW
					herpes simplex virus.
					XX
					OS Homo sapiens.
					PN W09420127-A.
					XX
					PD 15-SEP-1994.
					XX
					PF 04-MAR-1994;
					XX
					94WO-US02353.
					PR 05-MAR-1993;
					PR 04-JUN-1993;
					PR 29-NOV-1993;
					XX
					(CYTE-) CYTEL CORP.
					XX
					PT Grey HM, Kast WM, Sette A, Sidney J;

WPI: 1994-302678/37.
X Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
X for treatment or prophylaxis of cancer, virus infection or
X autoimmune diseases.
X
X disclosure; Page 80; 138PP; English.

WPI; 1994-302678/37.

Immunogenic peptide(s) having an HLA-A2.1 binding motif - used for treatment or prophylaxis of cancer, virus infection or autoimmune diseases.

Disclosure; Page 80; 138pp; English.

R73685-876 are potential peptide binders of HLA-A2.1 motif. Using motifs disclosed in the invention, these peptides were screened for further motifs. Only Peptides with binding affinity of at least 1% (binding affinity is expressed as an IC50 value) as compared to the standard peptide (R71293) in assays. This peptide has an binding value of 0.1500. The peptides of the invention can induce cytotoxic T lymphocytes which can react with target cells. They can be used for the treatment or prophylaxis of cancer, e.g. prostate cancer or lymphoma, etc.

CC similar compounds which may be useful for treating cancer or virally-
infected cells, or for diagnosis. The peptide and vaccines produced provide immunity to a high percentage of different ethnic groups, i.e. those with different HLA alleles.

Query	Match	Score	Length
Best Local Similarity	100.0%	17	9;
Matches	100	Pred. No.	2.1e+03;
Conservative	0	Mismatches	0;
XX	0	Indels	0;
SQ Sequence	9 AA;	Gaps	

Query	Match	Score	Length
Qy	1 KIFGSLAFL 9	17	9;
Db	1 kifgslaf 9	Pred. No.	2.1e+03;
RESULT	3	Mismatches	0;
W36824		Indels	0;
TD		Gaps	

Sequence 9 AA;

CC side-reactions and short peptide derivatives of TCR are more economical
 CC to produce than TCR itself, particularly when expressed as a
 CC single-chain molecule rather than as a dimer.
 XX Sequence 9 AA;

Query Match 100.0%; Score 43; DB 19; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIFGSLAFL 9
 ||||| |||||
 Db 1 kifgslaf 9

RESULT 4
 W77131 ID W77131 standard; peptide: 9 AA.

XX AC W77131;
 XX DT 16-NOV-1998 (first entry)

XX DE HER-2/neu synthetic peptide epitope 1.

XX KW Tyrosinase; tyrosinase cytotoxic lymphocyte response;

XX cytotoxic T lymphocyte; cysteine-depleted; melanoma.

XX OS Synthetic.

XX PN W09833810-A2.

XX PD 06-AUG-1998.

XX PF 29-JAN-1998; 98WO-US01592.

XX PR 30-JAN-1997; 97US-0037781.

XX PA (UYVI-) UNIV VIRGINIA PATENT FOUND.

XX PI Engelhardt VH, Hunt DF, Kittlesen D, Slingluff CL;

XX DR WPI; 1998-437388/37.

XX Disease specific immunogen - comprises disease specific cytotoxic T

PT lymphocyte epitope used to elicit melanoma specific CTL response

XX Disclosure; Page 27; 93pp; English.

XX The peptide epitope W77119-W77138 were created for human tumour-specific

CC cytotoxic T lymphocyte response. These peptides are are cysteine-

CC depleted mutants of a native disease-specific CTL epitope. The cysteine-

CC depleted CTL epitopes elicit a stronger or more specific CTL response

CC than the native epitope. The epitopes can be used in a disease-specific

CC immunogen to protect a mammal against disease in particular melanomas.

CC The peptides may also be used to screen a sample for the presence of

CC an antigen with the same epitope, or with a different cross-reactive

CC epitope.

XX Sequence 9 AA;

Query Match 100.0%; Score 43; DB 19; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.1e+05;

Matches 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
 ||||| |||||

Db 1 kifgslaf 9

RESULT 5
 W70057

W78859 ID W78859 standard; peptide: 9 AA.
 XX AC W78859;
 XX DT 17-NOV-1998 (first entry)

XX DE HER-1/neu protein fragment 369-377.

XX KW Microparticle; delivery: polymeric matrix; autoantigen; tumour antigen;

XX class II associated peptide; pathogen; gene therapy; genetic disease;

XX infection; downregulation; immune response.

XX Homo sapiens.

OS Synthetic.

XX PN W09831398-A1.

XX PD 23-JUL-1998.

XX PF 22-JAN-1998; 98WO-US01499.

XX PR 06-JAN-1998; 98US-0003253.

XX PR 22-JAN-1997; 97US-078547.

XX PA (PANG-) PANGAEA PHARM INC.

XX PI Curley JM, Hedley ML, Langer RS, Lunsford LB;

XX DR WPI; 1998-422556/36.

XX Disclosure; Page 10; 101pp; English.

XX PS New preparations of microparticles - comprising a synthetic polymer

PT matrix and nucleic acid comprising an expression vector for use in

PT gene therapy

XX Disclosure; Page 10; 101pp; English.

XX PS A microparticle preparation (MP) has been developed, consisting of

CC microparticles having a diameter of less than 100 μm. The MP comprises

CC (a) a polymeric matrix (PM) consisting of one or more synthetic polymers

CC having a solubility in water of less than 1 mg/ml; and (b) an expression

CC vector selected from RNA molecules (at least 50% which are closed

CC circles) or circular plasmid DNA (at least 50% of which are supercoiled).

CC Also described is a MP of at most 20 microns in diameter, comprising:

CC (a) a PM comprising an expression control sequence operatively

CC linked to a coding sequence, where the coding sequence encodes an

CC expression product selected from: (1) a polypeptide at least 7 amino

CC acids in length, having a sequence identical to the sequence of: (1) a

CC fragment of a naturally-occurring mammalian protein; or (2) a fragment

CC of a naturally-occurring protein from an infectious agent which infects

CC a mammal; (2) a peptide having a length and sequence which permits it to

CC bind to an MHC class I or II molecule; and (3) the polypeptide or the

CC peptide linked to a trafficking sequence. W69763 to W69765, and W7893

CC to W7897 are peptide fragments for use in the present invention. The

CC MPs are highly effective vehicles for the delivery of polynucleotides

CC into phagocytic cells. They can be used for gene therapy, e.g. for

CC treating genetic diseases, infections or tumours or for downregulating

CC an immune response.

XX Sequence 9 AA;

Query Match 100.0%; Score 43; DB 19; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.1e+05;

Matches 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
 ||||| |||||

Db 1 kifgslaf 9

RESULT 6
 W70057

ID	W70057 standard; peptide; 9 AA.	ID	Y10495 standard; Peptide; 9 AA.
XX		XX	Y10495;
AC		AC	Y10495;
XX		XX	12-MAY-1999 (first entry)
DT		DT	12-MAY-1999
XX		XX	HLA Class I motif peptide SEQ ID NO:425.
DE		DE	
XX		KW	Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;
KW		KW	immunisation; tumour; infectious disease; immunotherapy; cancer;
KW		KW	malignant melanoma; viral disease; hepatitis; AIDS.
KW		XX	
KW		OS	Synthetic.
KW		XX	Homo sapiens.
OS		PN	WO9002183-A2.
OS		XX	
Homosapiens.		PD	21-JAN-1999.
PN	WO0833888-A1.	XX	
XX		PF	10-JUL-1998;
PD		XX	98WO-US14289.
XX		PR	10-DEC-1997;
PF	30-JAN-1998;	PR	10-JUL-1997;
XX	98WO-US01959.	XX	97US-0988320.
PR	31-JAN-1997;	XX	97CA-2209815.
XX	97US-0036696.	PA	(CTLI-) CTL IMMUNOTHERAPIES CORP.
PA	(EPTM-) EPIMMUNE, INC.	XX	
PA		PI	Kuendig TM, Simard JJ;
PI		XX	
PI	Cells E, Sette A, Sidney J, Southwood S, Tsai V;	DR	WPI; 1999-120514/10.
XX		XX	
DR	WPI; 1998-437445/37.	PT	Inducing a cytotoxic T lymphocyte response - by maintaining a level
XX		PT	of antigen in the lymphatic system of a mammal so as to provide a
PT	immunogenic peptide(s) from antigen that binds class I major	PT	sustained CTL response, used to treat, e.g. AIDS
PT	histocompatibility complex molecules with pre-treated antigen	XX	
PT	presenting cells	PS	Disclosure; Page 43; 199pp; English.
XX		XX	
PS	Example 7; Page 77; 104pp; English.	CC	The present invention describes a method of inducing and/or sustaining
XX		CC	an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The
CC	Sequences shown in W70053 to W70075 represent peptides derived from	CC	method comprises: (a) delivering an antigen to the mammal at a level to
CC	HER-2/neu (cerB-2) antigen. The peptides can bind to a human leukocyte	CC	induce an immunological CTL response in the mammal; and (b) maintaining
CC	antigen (HLA), HLA-A2.1 and are used to exemplify the method of	CC	the level of the antigen in the mammal's lymphatic system to maintain
CC	invention of producing antigen-specific cytotoxic T cells (CTLs) in	CC	the immunological CTL response. The method can be used for the delivery of
CC	vitro. The method comprises contacting immunogenic peptides from an	CC	e.g. a differentiation antigen, a tumour-specific multiligneage antigen,
CC	antigen that binds class I major histocompatibility complex (MHC)	CC	an embryonic antigen, an oncogene, a mutated tumour-suppressor
CC	molecules with antigen presenting cells (APCs), pretreated with	CC	gene antigen, or a viral antigen. They can be used for the treatment of
CC	pretreatment growth factor, and incubating the APCs with purified CD8	CC	CC disease such as cancer, e.g. malignant melanoma or infectious disease,
CC	cells in the presence of at least 2 incubation growth factors, thereby	CC	CC e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery
CC	producing antigen-specific CTLs. A method for specifically killing	CC	CC to the lymphatic system provides for potent CTL stimulation that takes
CC	target cells in a human patient is also provided which comprises	CC	CC place in the milieu of the lymphoid organ, and it sustains stimulation
CC	obtaining a fluid sample containing CTLs from a patient, contacting the	CC	CC that is necessary to keep CTL active, cytotoxic and recirculating
CC	cytotoxic T cells with APCs pretreated with pre-treatment growth factors,	CC	CC through the body. Y10071 to Y10639 represent examples of peptide
CC	where the APCs comprise class I MHC molecules. The pretreated APCs are	CC	CC antigens given in the present invention.
CC	incubated with the cytotoxic growth factors, thereby producing activated	XX	
CC	CTLs which are contacted with a carrier to form a composition. The	Sequence	Sequence 9 AA;
CC	composition can then be administered to the patient. The activated CTLs	Qy	1 KIFGSLAFL 9
CC	can be used for treating cancers, immune disorders, viral infections,	Best Local Similarity	100.0%;
CC	CC AIDS, hepatitis, bacterial infection, fungal infection, malaria or	Matches	Score 43;
CC	CC tuberculosis.	Indels	DB 20;
XX	Sequence 9 AA;	Mismatches	Length 9;
Qy	1 KIFGSLAFL 9	0;	0;
Db	1 kifgslaf1 9	0;	0;
RESULT	8		
Y98846			
ID	Y98846 standard; Peptide; 15 AA.		
AC	Y98846;		
XX			
DN	07-AUG-2000 (first entry)		
XX			
RESULT	7		
Y10495			
Db			
RESULT	8		
Y98846			
ID	Y98846 standard; Peptide; 15 AA.		
AC	Y98846;		
XX			

DE	HLA class II binding antigen epitope peptide #35.
XX	Human leucocyte antigen: HLA class II; antigen epitope; pharmaceutical; immune response; chronic viral disease; cancer; autoimmune disease; rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS; allograft rejection; allergy; lyme disease; hepatitis; prostate cancer; glomerulonephritis; food hypersensitivity; malaria.
XX	Unidentified.
OS	W09961916-A1.
XX	PN
XX	PD
XX	02-DEC-1999.
XX	PPF
XX	28-MAY-1999; 99WO-US12066.
XX	PPF
XX	PR
XX	29-MAY-1998; 98US-0087192.
XX	PA
XX	(EPIM-) EPIMMUNE INC.
XX	Sette A, Southwood S, Sidney J;
XX	WPI: 2000-097143/08.
XX	DR
XX	PR
XX	PT
XX	PS
XX	PS
XX	Claim 1; Page 40; 60pp; English.
XX	XX
CC	The present invention relates to a new pharmaceutical composition comprising a unit dose form of a peptide, or analogue, comprising an epitope selected from those represented by peptides Y98812-Y99339 which are derived from various antigens for various human leucocyte antigen class DR molecules, representative of the world wide population. The peptide/analogue binds to an HLA class II molecule at an IC-50 of less than or equal to 1,000 nM. The pharmaceutical can be used to induce a helper T cell response. The pharmaceutical focuses the immune response towards selected determinants and could therefore be used in cases of chronic viral diseases and cancer. Examples of diseases that can be treated using the peptide containing pharmaceutical include autoimmune diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia gravis), allograft rejection, allergies, lyme disease, hepatitis, post-streptococcal endocarditis or glomerulonephritis and food hypersensitivities. The peptide epitopes can be used to enhance immune responses against other immunogens administered with the peptides. Diseases which can be treated using immunogenic mixtures include prostate cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be used to make monoclonal antibodies useful as potential diagnostic or therapeutic agents. The peptides may also be useful as diagnostic reagents, for example, to determine the susceptibility of an individual to a treatment regimen. Also, the peptides may be used to predict which individuals will be at substantial risk of developing chronic infection the selection of appropriate T and B cell epitopes should allow the development of epitope based vaccines particularly towards conserved epitopes of pathogens which are characterized by high sequence

XX SQ Sequence 15 AA;

QY	1	KIFGSLAFL	9
Db	3	kifgslaf1	11
RESULT	9		
008/22			
ID	ROB222	standard:	protein: 624 AA.

XX	R08222;
AC	
XX	
DT	06-MAR-1991 (first entry)
XX	
DE	Extracellular portion of the human epidermal growth factor receptor 2
XX	
KW	Human epidermal growth factor receptor 2; HER2; vaccine; cancer.
XX	
KW	Homo sapiens.
OS	
XX	
FH	KEY
FT	Region
FT	22..32
FT	/label= epitope
FT	/note= "potential T-cell epitope"
FT	74..84
FT	/label= epitope
FT	/note= "potential T-cell epitope"
FT	113..130
FT	/label= epitope
FT	/note= "potential T-cell epitope"
FT	187..197
FT	/label= epitope
FT	/note= "potential T-cell epitope"
FT	305..315
FT	/label= epitope
FT	/note= "potential T-cell epitope"
FT	322..353
FT	/label= epitope
FT	/note= "potential T-cell epitope"
FT	374..385
FT	/label= epitope
FT	/note= "potential T-cell epitope"
FT	398..408
FT	/label= epitope
FT	/note= "potential T-cell epitope"
FT	413..443
FT	/label= epitope
FT	/note= "potential T-cell epitope"
FT	518..529
FT	/label= epitope
FT	/note= "potential T-cell epitope"
XX	W09014357-A.
PN	
XX	29-NOV-1990.
PD	
XX	18-MAY-1990; 90W0-US0697.
XX	19-MAY-1989; 89US-0354319.
XX	
PA	(GETH) GENENTECH INC.
XX	
P1	Hudziak RM, Shepard HM, Ulrich A;
XX	
WPI	1990-375946/50.
DR	

XX HER2 extracellular domain used as vaccine - comprises sequence of
PT at least 9 amino acid(s) prep'd, using expression vector of DNA
PR isolated from human epidermal growth factor receptor
PS Disclosure; Fig 13; 49pp; English.
XX
CC This claimed sequence is free of transmembrane or intracellular
CC portions of the HER2 mol. The protein is antigenic in animals.
CC Fragment comprising at least 9 amino acids open several
CC possibilities for further research and a broad range
CC of potential therapeutic applications, e.g. for the treatment of
CC mammary gland adenocarcinoma and other cancers.
CC Sequence 624 AA;
XX

Query Match	100.0%	Score 43;	DB 11;	Length 624;	Qy	1 KIFGSLAFL 9
Best Local Similarity	100.0%	Pred. No. 0.4;				
Matches	9; Conservative	0; Mismatches	0;	Indels 0;	Gaps 0;	
Qy	1 KIFGSLAFL 9					
Db	348 kifgslafL 356					
RESULT 10						
W19764	standard; Protein; 782 AA.					
XX						
XX	17-SEP-1997 (first entry)					
XX	Her-2-GM-CSF immunostimulant fusion protein.					
DE						
KW	Her2-GM-CSF; granulocyte macrophage colony stimulating factor;					
KW	growth factor receptor; oncogene; immunostimulant; cancer;					
KW	KW therapy.					
XX						
OS	Homo sapiens.					
XX						
FH	Location/Qualifiers					
FT	Key					
FT	Protein	1..653				
FT		/label= Her2				
FT		654..655				
FT		/label= Linker				
FT	Protein	656..782				
FT		/label= GM-CSF				
XX	W09724438-A1.					
XX						
XX	10-JUL-1997.					
XX						
PF	23-DEC-1996;	96WO-US20241..				
XX	28-DEC-1995;	95USP-0579823..				
XX						
PA	(ACTI-1) ACTIVATED CELL THERAPY INC.					
XX						
PI	Laus R, Ruegg CL, Wu H;					
XX						
DR	WPI: 1997-363674/33.					
DR	N-PSDB: "72225.					
XX						
PT	Potent APC that activates T-cells to give multivalent cellular immune response - can also induce a cytotoxic T-cell response in a vertebrate subject					
XX						
PS	Disclosure; Fig 8; 45DP; English.					
XX						
CC	A fusion protein (W19764) comprises Her2 (a growth factor receptor that is overexpressed in breast, ovarian can other cancer cells) and granulocyte-macrophage colony stimulating factor (GM-CSF). It is the expression product of a nucleic acid molecule (T7225) prepd. by PCR amplification of Her2 cDNA from a breast cancer cell line and fusion to GM-CSF cDNA. Fusion expression vectors can be used to transfect mammalian and insect cells. The Her2-GM-CSF fusion protein is used to generate anti-Her2 immunity. Tumour cells are eliminated by cytotoxic T lymphocytes activated in vivo or in vitro by exposure to antigen-presenting cells exposed to the fusion protein.					
CC	Sequence 782 AA;					
XX						
PS	Query Match 100.0%; Score 43; DB 18; Length 782;					
PS	Best Local Similarity 100.0%; Pred. No. 0.51;					
PS	Matches 0; Mismatches 0;					
PS	Indels 0; Gaps 0;					
PS	RESULT 11					
XX	Y44993 standard; Protein; 951 AA.					
XX						
AC	Y44993;					
XX	23-MAY-2000 (first entry)					
DE	DC8scFv-erbB2EC fusion protein containing tetramerisation domain.					
XX	DC8 scFv; single-chain variable fragment; erbB2EC; extracellular domain;					
KW	human; fusion construct; tetramerisation domain; constant domain;					
KW	heteromimibody; multifunctional compound;					
KW	immunoglobulin; cytosolic; immunostimulatory; diagnosis;					
KW	antiproliferative; prevention; treatment; malignant; haematopoietic cell;					
KW	lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma.					
XX						
OS	Chimeric - Unidentified.					
OS	Chimeric - Homo sapiens.					
XX						
Key	Location/Qualifiers					
FT	1..19					
FT	Peptide					
FT		/label= Leader_sequence				
FT	Region	20..127				
FT		/label= DC8scFv_Light_chain_variable_region				
FT	Region	128..142				
FT		/label= Glycine-Serine-linker				
FT	Region	143..254				
FT		/label= DC8scFv_heavy_chain_variable_region				
FT	Region	256..266				
FT		/note= "5' end of human IgG3 upper hinge region with additional residues"				
FT	Domain	267..305				
FT		/label= Human_p53_tetramerisation_domain				
FT	Peptide	306..312				
FT		/label= Short_peptide_linker				
FT	Domain	313..945				
FT		/label= erbB2EC_domain				
FT	Region	946..951				
FT		/label= His_tag				
XX	WO200006605-A2.					
XX	10-FEB-2000.					
XX	99WO-EP05416.					
XX	28-JUL-1998;					
XX	98EP-0114082.					
PA	(MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.					
XX	New multifunctional compounds useful for preventing and/or treating malignant cell growth and for detection and diagnosis -					
PT	Example 9; Fig 9; 166pp; English.					
XX						
CC	The patent discloses heteromimibodies which are multifunctional compounds producible in a mammalian host cell as a secretable and fully functional heterodimer of two polypeptide chains, where one of the polypeptide chains comprises a CH1-domain (constant domain of an immunoglobulin heavy chain) and the other chain comprises CL-domain (constant domain of an immunoglobulin light chain). The polypeptide chains further comprise,					

fused to the constant domains at least two (poly)peptides having different receptor or ligand functions, where further at least two of the different (poly)peptides lack an intrinsic affinity for one another and are linked via the constant domains. The heteromimobodies have cytostatic, immunostimulatory, anti-leukaemia and anti-proliferative activities. These compounds can be used for diagnosing, preventing and treating malignant cell growth related to malignancies of haematopoietic cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas, melanomas and sarcomas.

The present sequence is a fusion protein comprising DC8 single-chain Fv (scFv) fragment at the N-terminus, extracellular domain of human erb2 at the C-terminus and a tetramerisation domain between them. This construct was prepared to find out whether an oligomerisation domain characterised in bacterial expression system is applicable for expression of fully functional and secretable recombinant protein in mammalian host cells. This tetrameric construct was not expressed as secretable and fully functional protein in mammalian cells. Hence general applicability of the tetramerisation domain for oligomerisation strategies in mammalian cells was ruled out.

Sequence 951 AA;

Query Match 100.0%; Score 43; DB 21; Length 951;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 K1FGSLAFL 9
Db 660 k1fgs1af1 668

RESULT 12

W01111 standard; Protein; 1255 AA.
XX
AC W01111;
XX
DT 01-JAN-1997 (first entry)

XX
DE HER-2/neu protein.
XX
KW HER-2/neu; c-erbB1; p185; oncogene; tyrosine protein kinase;
KW breast cancer; ovarian cancer; colon cancer; lung cancer;
KW prostate cancer; immunisation; tumour; vaccine; vector.
XX
OS Homo sapiens.

XX
FH Location/Qualifiers
Domain 676..1255
/label= "Intracellular_domain
/note= "claimed domain, useful for immunisation"

PN W09630514-A1.

XX
PD 03-OCT-1996.XX
PF 28-MAR-1996; 96WO-US01689.XX
PR 31-MAR-1995; 95US-0414417.

PA (UNIW) UNIV WASHINGTON.

XX
PI Cheever MA, Disis ML;XX
DR WPI: 1996-455361/45.

DR N-PSDB; T40739.

XX
PT DNA encoding HER-2/neu poly:peptide(s) - used for prevention or

PT treatment of malignancies with which the HER-2/neu oncogene is

PT associated

XX
PS Claim 2; Page 56-61; 71pp; English.

XX Human HER-2/neu protein (W01111), also called p185 or c-erbB2, is the product of the HER-2/neu oncogene (see also T40739). The protein is over-expressed in various cancers including breast, ovarian, colon, lung and prostate. The intracellular domain of the protein can be used to immunise an animal against a malignancy with which the oncogene is associated. The polypeptide can be produced in transformed host cells for use in immunisation. Alternatively, animal cells are transfected in vivo or ex vivo with a viral vector that directs expression of the polypeptide.

SQ Sequence 1255 AA;

Query Match 100.0%; Score 43; DB 17; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 K1FGSLAFL 9
Db 369 k1fgs1af1 377

RESULT 13

W92406 standard; Protein; 1255 AA.
XX
ID W92406
AC W92406;
XX
DT 21-APR-1999 (first entry)

XX
DE Human HER-2/neu oncogene protein.

XX
KW HER-2/neu; oncogene; immune response; T cell; B cell; immunisation;
KW malignancy; treatment; tumour.
XX
OS Homo sapiens.

XX
FH Location/Qualifiers
Region 676..1255
/note= "region which elicits immune response"

XX
XX
PD 09-FEB-1999.

XX
PF 01-APR-1996;
XX
PR 01-APR-1996;
PR 17-MAR-1993;
PR 12-AUG-1993;
PR 31-MAR-1995;
XX
PA (UNIW) UNIV WASHINGTON.

XX
DR WPI: 1999-152335/13.

DR N-PSDB; X01912.

XX
PT Use of HER-2/neu polypeptides - for eliciting an immune response to an HER-2/neu associated malignancy, particularly for treating or preventing tumours

XX
PI Cheever MA, Disis ML;XX
PS Claim 3; Column 31-38; 26pp; English.

XX
CC This sequence represents the human HER-2/neu oncogene protein. A fragment of this protein is used in a method for eliciting or enhancing an immune response to HER-2/neu protein. The polypeptide can stimulate T cells and B cells to produce an immune response to the HER-2/neu protein. The method can be used for immunisation against a malignancy in which the HER-2/neu oncogene is associated and in the treatment of an existing tumour, or to prevent tumour occurrence or reoccurrence.

FT /label= insertion_region
 FT /note= "suitable for foreign epitope insertion"
 FT Region
 FT /label= insertion_region
 FT /note= "suitable for foreign epitope insertion"
 FT Domain
 FT /label= C-terminal_domain
 XX
 PN WO200020027-A2.
 XX
 PD 13-APR-2000.
 XX
 PF 05-OCT-1999; 99WO-DK00525.
 XX
 PR 05-OCT-1998; 98DK-0001261.
 PR 20-OCT-1998; 98US-0105011.
 XX
 PA (MEBI-) M & E BIOTECH AS.
 XX
 PI Steinaa L, Mouritsen S, Nielsen KG, Haaning J, Leach D, Dalum I;
 PI Gautam A, Birk P, Karisson G;
 XX
 DR WPI: 2000-349917/30.
 DR N-PSDB; A09455.
 XX
 PT Inducing immune responses to weakly immunogenic, tumor associated
 PR peptide antigens for the treatment of breast and prostate cancer
 XX
 PS Claim 62; Page 193-198; 220pp; English.
 XX
 CC This is the human heregulin 2 (Her2) sequence. Immunogenic analogues of
 CC Her2 can be used in the claimed method as an autovaccine to induce a CTL
 CC response. Subdominant CTL epitopes, antibody binding regions and
 CC cysteine residues involved in disulfide bonds are preserved in the
 CC immunogenized forms. Regions suitable for the insertion of foreign T
 CC helper epitopes were identified (see features table). The method
 CC is used for inducing immune responses against weakly immunogenic
 CC cell-associated peptide antigens (PA) such as those associated with
 CC cancers (self-proteins), e.g. human prostate specific membrane antigen
 CC (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b).
 CC The method comprises effecting simultaneous presentation by antigen
 CC producing cells (APCs) of the animals immune system of: (1) at least 1
 CC CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1
 CC B-cell group derived from the cell-associated PA; and (2) at least 1
 CC first T helper cell group which is foreign to the animal. Analogues of
 CC human PSM, human Her2 and human/murine FGF8b comprising a substantial
 CC part of all known and predicted CTL and B-cell epitopes of the respective
 CC PA and including at least one foreign T helper epitope are also claimed.
 CC The method is used to treat prostate, prostate/breast or breast cancer
 CC when the PA is human PSM, FGF8b and Her2, respectively.
 XX
 S0 Sequence 1255 AA;
 XX
 Query Match 100.0%; Score 43; DB 21; Length 1255;
 Best Local Similarity 100.0%; Pred. No. 0.83;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KIFGSLAFL 9
 Db 369 kifgslaf 377

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GenCore version 4.5
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run on: November 14, 2000, 11:54:42 ; Search time 12.27 Seconds
(without alignments)
12.294 Million cell updates/sec

title: US-09-277-074-10
perfect score: 43
equence: 1 KIFGSLAFL 9

scoring table: BIOSUM62
GapoP 10.0 , Gapext 0.5

searched: 164575 seqs, 1676186 residues

total number of hits satisfying chosen parameters: 164575

minimum DB seq length: 0
maximum DB seq length: 2000000000

post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

database : Issued_Patents_AA.*

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3: /cgn2_6/podata/2/1aa/6_COMB_pep:
4: /cgn2_6/podata/2/1aa/PCMV_COMB_pep:
5: /cgn2_6/podata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Query Score	Match Length	DB ID	Description
1	43	100.0	9	US-08-467-083-27
2	43	100.0	9	US-08-787-567-70
3	43	100.0	9	US-08-414-417B-27
4	43	100.0	9	US-08-486-348A-27
5	43	100.0	9	US-08-468-545B-27
6	43	100.0	9	US-08-202-516-18
7	43	100.0	9	US-08-855-16A15-10
8	43	100.0	9	PCT-US55-16A15-10
9	43	100.0	16	US-08-467-083-62
10	43	100.0	16	US-08-414-417B-62
11	43	100.0	16	US-08-186-348A-62
12	43	100.0	16	US-08-168-545B-62
13	43	100.0	16	US-08-466-680B-62
14	43	100.0	624	US-08-212-108-1
15	43	100.0	782	US-09-146-283-4
16	43	100.0	782	US-08-519-823A-4
17	43	100.0	1255	US-08-167-083-68
18	43	100.0	1255	US-08-414-417B-68
19	43	100.0	1255	US-08-484-438-8
20	43	100.0	1255	US-08-186-348A-68
21	43	100.0	1255	US-08-225-101-2
22	43	100.0	1255	US-08-168-545B-68
23	43	100.0	1255	US-08-519-823A-4
24	43	100.0	1255	US-08-166-680B-68
25	30	69.8	269	US-08-118-210-64
26	30	69.8	269	US-08-123-389C-1
27	30	69.8	790	US-08-181-863-1
28	30	69.8	790	US-08-186-596A-1
29	30	69.8	792	US-08-326-670A-2
30	30	69.8	792	US-08-537-361E-2
31	30	69.8	792	US-08-537-361E-6
32	29	67.4	15	US-08-467-083-36
33	29	67.4	15	US-08-414-417B-36
34	29	67.4	15	US-08-486-348A-36
35	29	67.4	15	US-08-468-545B-36
36	29	67.4	15	US-08-466-680B-36
37	29	67.4	24	US-08-103-445-21
38	29	67.4	24	US-08-161-690B-21
39	29	67.4	457	5447867-1
40	29	67.4	711	US-08-772-270A-12
41	28	65.1	182	US-08-538-823-5
42	28	65.1	185	US-08-233-389C-1
43	28	65.1	185	US-08-801-863-1
44	28	65.1	185	US-08-186-596A-1
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ALIGNMENTS

RESULT 1
US-08-467-083-27
Sequence 27, Application US/08467083
Patent No. 5726023
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
DISLIS, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH HER-2/NEU ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467-083
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/414,417
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010-448C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-4900
TELEFAX: (206) 682-6031
TELEX: 3723836 STEEDEBERRY
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPLOGY: linear
US-08-467-083-27

Query Match 100.0%; Score 43; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9
 Db 1 KIFGSLAFL 9

RESULT ²
 US-08-787-547-70
 ; Sequence 70, Application US/08787547
 ; Patent No. 5783567

GENERAL INFORMATION:
 ; APPLICANT: Hedley, Mary Lynne
 ; APPLICANT: Curley, Joanne M.
 ; APPLICANT: Langer, Robert S.
 ; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
 ; NUMBER OF SEQUENCES: 107
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson, P.C.
 ; STREET: 225 Franklin Street
 ; STATE: Boston
 ; COUNTRY: MA
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows95
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/787,547
 ; FILING DATE: 22-JAN-1997
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fraser, Janis K.
 ; REGISTRATION NUMBER: 34,819
 ; REFERENCE/DOCKET NUMBER: 08191/003001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-542-5070
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 70:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Peptide
 ; US-08-787-547-70

Query Match 100.0%; Score 43; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9
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 US-08-414-417B-27
 ; Sequence 27, Application US/08414417B
 ; Patent No. 5801005

GENERAL INFORMATION:
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: Disis, Mary L.
 ; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
 ; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
 ; NUMBER OF SEQUENCES: 69
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; ZIP: 98104-7092

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, version #1.25

CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/414,417B
 ; FILING DATE: 31-MAR-1995 ✓
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sharkey, Richard G.
 ; REGISTRATION NUMBER: 32,629
 ; REFERENCE/DOCKET NUMBER: 920010.448C2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 27:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; US-08-414-417B-27

Query Match 100.0%; Score 43; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT ⁴
 US-08-486-348A-27
 ; Sequence 27, Application US/08486348A
 ; Patent No. 5846538

GENERAL INFORMATION:
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: Disis, Mary L.
 ; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
 ; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
 ; NUMBER OF SEQUENCES: 69 ✓
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Seed and Berry LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; ZIP: 98104-7092

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, version #1.25

CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/486,348A
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sharkey, Richard G.
 ; REGISTRATION NUMBER: 32,629
 ; REFERENCE/DOCKET NUMBER: 920010.448C6
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900

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; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; 'TOPOLogy: linear
US-08-468-348A-27

Query Match 100.0% Score 43; DB 2; Length 9;
Best local Similarity 100.0% Pred. No. 1.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 KIFGSLAFL 9

RESULT 5
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; GENERAL INFORMATION:
; Patent No. 5876712
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSTS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; NUMBER OF SEQUENCES: 69
; NUMBER OF SEQUENCES: 69
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; APPLICATION NUMBER: US/08468545B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; REFERENCE/DOCKET NUMBER: 32, 629
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REFERENCE/DOCKET NUMBER: 920010.448C5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; 'TOPOLogy: linear
US-08-468-545B-27

Query Match 100.0% Score 43; DB 2; Length 9;
Best Local Similarity 100.0% Pred. No. 1.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9
Db 1 KIFGSLAFL 9

RESULT 6
US-08-902-516-18
; Sequence 18, Application US/08902516
; Patent No. 589132
; GENERAL INFORMATION:
; APPLICANT: SOO HOO, WILLIAM
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
; COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
; RESPONSE USING SAME
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902.516
; FILING DATE: 29-JUL-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Kathryn A.
; REGISTRATION NUMBER: 31, 815
; REFERENCE/DOCKET NUMBER: P-IM 2442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)535-9001
; TELEFAX: (619)535-8949
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-902-516-18

Query Match 100.0% Score 43; DB 2; Length 9;
Best Local Similarity 100.0% Pred. No. 1.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9
Db 1 KIFGSLAFL 9

RESULT 7
US-08-466-680B-27
Sequence 27, Application US/08466680B
; Patent No. 607512
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; NUMBER OF SEQUENCES: 69
; NUMBER OF SEQUENCES: 69
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/4666, 6803
 FILING DATE: 06 - JUN - 1995
 CLASSIFICATION: 4.24
 ATTORNEY / AGENT INFORMATION:
 NAME: Sharkey, Richard G.
 REGISTRATION NUMBER: 32, 629
 REFERENCE/DOCKET NUMBER: 920010.448C4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-466-680B-27

Query Match 100.0%; Score 43; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 KIFGSLAFL 9
 Db 1 KIFGSLAFL 9

RESULT 9
 US-08-467-083-62
 Sequence 62, Application US/08467083
 Patent No. 5726023
 GENERAL INFORMATION:
 APPLICANT: Cheever, Martin A.
 APPLICANT: Disis, Mary L.
 TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
 TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
 TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
 TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
 NUMBER OF SEQUENCES: 68
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Seed and Berry
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: US
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25.
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467, 083
 FILING DATE: 06 - JUN - 1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/414, 417
 FILING DATE: 06 - JUN - 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Sharkey, Richard G.
 REGISTRATION NUMBER: 32, 629
 REFERENCE/DOCKET NUMBER: 920010.448C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 TELEX: 3723836 SIEBANBERRY
 INFORMATION FOR SEQ ID NO: 62:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-467-083-62

Query Match 100.0%; Score 43; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.0076;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 KIFGSLAFL 9
 Db 1 KIFGSLAFL 9

RESULT 10
 US-08-414-417B-62
 Sequence 62, Application US/08414417B
 Patent No. 5801005
 GENERAL INFORMATION:
 APPLICANT: Cheever, Martin A.
 APPLICANT: Disis, Mary L.
 TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
 TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
 TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
 TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED

Query Match 100.0%; Score 43; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;

```

; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414.417B
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-0311
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-414-417B-62

Query Match 100.0%; Score 43; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 K1FGSLAFL 9
Db 1 K1FGSLAFL 9

RESULT 11
US-08-486-348A-62
; Sequence 62, Application US/08486348A
; Patent No. 5846538
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; NUMBER OF SEQUENCES: 69
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468.545B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-0311
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-468-545B-62

Query Match 100.0%; Score 43; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 K1FGSLAFL 9
Db 1 K1FGSLAFL 9

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RESULT 13
US-08-466-6380B-62
; Sequence 62, Application US/08466660B
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/4666.680B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 9200010.448C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-466-6380B-62

Query Match 100.0%; Score 43; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0076; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9
Db 1 KIFGSLAFL 9

RESULT 14
US-08-422-108-1
; Sequence 1, Application US/08422108
; GENERAL INFORMATION:
; APPLICANT: Hudzak, Robert M.
; APPLICANT: Shepard, H. Michael
; TITLE OF INVENTION: HER2 EXTRACELLULAR DOMAIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

Query Match 100.0%; Score 43; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0076; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9
Db 1 KIFGSLAFL 9

RESULT 14
US-08-422-108-1
; Sequence 1, Application US/08422108
; GENERAL INFORMATION:
; APPLICANT: Hudzak, Robert M.
; APPLICANT: Shepard, H. Michael
; TITLE OF INVENTION: HER2 EXTRACELLULAR DOMAIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

Query Match 100.0%; Score 43; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0076; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9
Db 1 KIFGSLAFL 9

RESULT 15
US-09-146-283-4
; Sequence 4, Application US/09146283
; GENERAL INFORMATION:
; APPLICANT: Ruegg, Curt L.
; APPLICANT: Wu, Hongyu
; TITLE OF INVENTION: Immunostimulatory Compositions
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave. Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/146,283
; FILING DATE: 03-SEPT-1998
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Judge, Linda R.
; REGISTRATION NUMBER: 42,702
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 782 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: homo sapiens

INDIVIDUAL ISOLATE: GM-CSF-Her-2 fusion protein; Fig. 8

US-09-146-283-4

Query Match 100.0%; Score 43; DB 2; Length 782;

Best Local Similarity 100.0%; Pred. No. 0.42;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIEGSLAFL 9
Db 369 KIEGSLAFL 377

Search completed: November 14, 2000, 11:55:00
Job time: 18 sec

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OM protein - protein search, using sw model

Run on: November 14, 2000, 11:54:42 ; Search time 13.48 Seconds
(without alignments)
42.370 Million cell updates/sec

Title: US-09-277-074-10
Perfect score: 43
Sequence: 1 KIFGSLAFL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 182106

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_65.1*
1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	1254	2 148161	p-185 precursor - protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - kinase-related transforming protein e
2	43	100.0	1255	1 A24571	p-185 precursor - protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - kinase-related transforming protein e
3	43	100.0	1260	1 TVRTNU	p-185 precursor - protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - kinase-related transforming protein e
4	36	83.7	356	2 T28747	p-185 precursor - protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - kinase-related transforming protein e
5	36	83.7	502	2 G71055	p-185 precursor - protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - kinase-related transforming protein e
6	34	79.1	298	2 S53849	p-185 precursor - protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - kinase-related transforming protein e
7	34	79.1	370	2 T48578	p-185 precursor - protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - kinase-related transforming protein e
8	34	79.1	540	2 S56215	p-185 precursor - protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - kinase-related transforming protein e
9	33	76.7	120	2 T16442	p-185 precursor - protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - kinase-related transforming protein e
10	33	76.7	449	2 F81954	p-185 precursor - protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - kinase-related transforming protein e
11	33	76.7	449	2 E81011	p-185 precursor - protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - kinase-related transforming protein e
12	32	74.4	157	2 S58038	p-185 precursor - protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - kinase-related transforming protein e
13	32	74.4	231	2 T20547	p-185 precursor - protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - kinase-related transforming protein e
14	32	74.4	298	2 S60649	p-185 precursor - protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - kinase-related transforming protein e
15	32	74.4	323	2 S05035	p-185 precursor - protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - kinase-related transforming protein e
16	32	74.4	454	2 T27040	p-185 precursor - protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - kinase-related transforming protein e
17	32	74.4	671	1 OKBOG	p-185 precursor - protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - kinase-related transforming protein e
18	32	74.4	686	1 S05702	p-185 precursor - protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - kinase-related transforming protein e
19	32	74.4	758	2 S62432	p-185 precursor - protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - kinase-related transforming protein e
20	32	74.4	1029	2 S56229	p-185 precursor - protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - kinase-related transforming protein e
21	31	72.1	138	2 A65187	p-185 precursor - protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - kinase-related transforming protein e
22	31	72.1	149	2 T28298	p-185 precursor - protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - kinase-related transforming protein e
23	31	72.1	232	2 H69173	p-185 precursor - protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - kinase-related transforming protein e
24	31	72.1	240	2 E70771	p-185 precursor - protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - kinase-related transforming protein e
25	31	72.1	251	2 S72791	p-185 precursor - protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - kinase-related transforming protein e
26	31	72.1	264	2 E72119	p-185 precursor - protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - kinase-related transforming protein e
27	31	72.1	326	2 B72282	p-185 precursor - protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - kinase-related transforming protein e
28	31	72.1	335	2 T20920	p-185 precursor - protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - kinase-related transforming protein e
29	31	72.1	343	2 T33989	p-185 precursor - protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - kinase-related transforming protein e

ALIGNMENTS

30	31	72.1	350	2 T28975	hypothetical prote
31	31	72.1	475	2 F71419	probable indole-3- hypothetical prote
32	31	72.1	505	2 T26764	probable transport
33	31	72.1	573	2 S60912	chloride channel, C
34	31	72.1	686	2 A45483	chloride channel, C
35	31	72.1	687	2 A57713	chloride channel, C
36	31	72.1	687	2 D57713	chloride channel, C
37	31	72.1	687	2 C57713	centromere-binding
38	31	72.1	956	2 S64449	hypothetical prote
39	31	72.1	965	2 T32574	T16G12.5 protein -
40	31	72.1	1483	2 S42839	T16G12.5 protein -
41	31	72.1	3848	2 T17414	TIPC protein - sli
42	31	72.1	4199	2 S76412	hypothetical prote
43	30.5	70.9	3351	2 T13812	lipophorin - fruit
44	30	69.8	51	2 T07326	hypothetical prote
45	30	69.8	77	2 A72256	hypothetical prote

RESULT 1					
I48161	p-185 precursor - golden hamster	C:Species: Mesocricetus auratus (golden hamster)	C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999	C:Accession: I48161	R:Nakamura, T.; Ishizaka, T.; Nagao, M.; Arai, M.; Yamazaki, Y.; Ishikawa Gene 140, 251-255, 1994
		A;Title: Cloning and activation of the syrian hamster neu proto-oncogene.		A;Reference number: I48161; MUID: 34193007	
		A;Status: preliminary; translated from GB/EMBL/DDJB		A;Molecule type: mRNA	
		A;Residues: 1-1254 <RES>		A;Cross-references: GB:D16295; NID:9493236; PIDN:BAA03801.1; PID:947595	
		C;Genetics:		A;Gene: neu	
		C;Superfamily: epidermal growth factor receptor; protein kinase homology		C;Keywords: ArP	
		F;718-983/Domain: protein kinase homology <KIN>		F;718-983/Region: protein kinase ATP-binding motif	
		F;726-734/Region: protein kinase homology <KIN>			

submitted to the Protein Sequence Database, April 2000

A; Reference number: Z24490
 A; Accession: T48578
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-570 <BEV>
 A; Cross-references: EMBL:AL163491
 A; Experimental source: Cultivar Columbia; BAC clone T31B5
 C; Genetics:
 A; Map position: 5
 A; Introns: 119/3
 A; Note: T31B5.130

A; Status: preliminary; nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; Residues: 1-502 <KAW>
 A; Cross-references: GB:AP000005; NID:93236132; PID:BA30241.1; PID:93257558
 A; Experimental source: strain Or3
 A; Note: this accession replaces an interim accession for a sequence replaced by GenBank
 A; Reference number: A71000; MUID:98344137
 C; Genetics:
 A; Gene: PH1141
 C; Superfamily: Pyrococcus horikoshii hypothetical protein PH1141

RESULT 5
 hypothetical protein PH1141 - Pyrococcus horikoshii
 C; Species: Pyrococcus horikoshii
 C; Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
 C; Accession: G71055
 R; Kavarabayasi, Y.; Sawada, M.; Horikawa, H.; Haino, Y.; Yamamoto, S.; Sekiro M.; Ohfuki, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushida, N.; Oguchi DNA Res. 5, 55-76, 1998
 A; Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
 A; Accession: G71055
 A; Status: preliminary; nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; Residues: 1-502 <KAW>
 A; Cross-references: GB:AP000005; NID:93236132; PID:BA30241.1; PID:93257558
 A; Experimental source: strain Or3
 A; Note: this accession replaces an interim accession for a sequence replaced by GenBank
 A; Reference number: A71000; MUID:98344137
 C; Genetics:
 A; Gene: PH1141
 C; Superfamily: Pyrococcus horikoshii hypothetical protein PH1141

Query Match 83.7%; Score 36; DB 2; Length 502;
 Best Local Similarity 87.5%; Pred. No. 8.5;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IFGSLAFL 9
 :|||||||
 Db 123 IFGSLAFL 130

RESULT 6
 ribosomal protein S3 - Acanthamoeba castellanii mitochondrion
 C; Species: mitochondrion Acanthamoeba castellanii
 C; Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 07-Dec-1999
 C; Accession: S53849
 R; Burger, G.; Planté, I.; Lonergan, K.M.; Gray, M.W.
 J. Mol. Biol. 245, 522-537, 1995
 A; Title: The mitochondrial DNA of the amoeboid protozoan, Acanthamoeba castellanii: comp
 A; Reference number: S53825; MUID:9514275
 A; Accession: S53849
 A; Status: nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; Residues: 1-298 <BUR>
 A; Cross-references: GB:U12386; PID:9562028; PID:9562053
 A; Experimental source: strain Neff; ATCC 30010
 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
 C; Genetics:
 A; Genome: mitochondrion
 A; Genetic code: SGC6
 C; Keywords: mitochondrion

Query Match 79.1%; Score 34; DB 2; Length 298;
 Best Local Similarity 87.5%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 8
 :|||||||
 Db 250 KAFGSLAFL 257

RESULT 7
 hypothetical protein T31B5.130 - Arabidopsis thaliana
 C; Species: Arabidopsis thaliana (mouse-ear cress)
 C; Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C; Accession: T48578
 R; Bevan, M.; Hibert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,

Query Match 79.1%; Score 34; DB 2; Length 540;
 Best Local Similarity 87.5%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IFGSLAFL 9
 :|||||||
 Db 459 IFGSLTFL 466

RESULT 9
 T16442 hypothetical protein F53B1.3 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
 C:Accession: T16442
 R:Miller, N.
 Submitted to the EMBL Data Library, November 1995
 A:Description: The sequence of *C. elegans* cosmid F53B1.
 A:Reference number: 218514
 A:Accession: T16442
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A: Molecule type: DNA
 A:Residues: 1-120 <MILD>
 A:Cross-references: ENB:U40953; NID:91072248; PID:91072249; PIDN:AAB52646.1; GSPDB:GN000022
 A:Experimental source: strain Bristol N2; clone F53B1
 A:Gene: CESP:F53B1.3
 A:Map position: X
 A:introns: 48/2; 71/3

RESULT 10
 FB:954 cytochrome B (EC 1.10.2.2) NMA0084 [Imported] - *Neisseria meningitidis* (group A strain 2
 C:Species: *Neisseria meningitidis*
 C:Accession: F81554
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, J.; Holroyd, S.; Jäger, K.; Leather, S.; Moulé, S.; Mungall, K.; Quail, M.A.; Rajandream, NATURE 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
 A:Reference number: A81775; MURID:2022556
 A:Accession: F81954
 A:Status: preliminary
 A: Molecule type: DNA
 A:Residues: 1-449 <PAR>
 A:Cross-references: GB:AL162753; GB:AL157959; NID:97379120; PIDN:CA83685.1; PID:9737913
 A:Experimental source: serogroup A, strain Z2491
 C:Genetics:
 A:Gene: petB; NMA0384
 C:Keywords: oxidoreductase

RESULT 11
 EB:0011 ubiquinol--cytochrome c reductase, cytochrome b NMB2052 [Imported] - *Neisseria meningitidis*
 C:Species: *Neisseria meningitidis*
 C:Accession: E81011
 R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haff, D.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; R.L.H.; Qin, H.; Yamamoto, J.; Gill, J.; Scarlato, V.; Masiognani, V.; Pizza, M.; Science 287, 1809-1815, 2000
 A:Authors: Grandi, C.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve

A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
 A:Reference number: A81000; MUID:20175755
 A:Accession: E81011
 A:Status: preliminary
 A: Molecule type: DNA
 A:Residues: 1-449 <TER>
 A:Cross-references: GB:AE002555; GB:AE002098; NID:97227310; PIDN:AAF42372.1; PID:97227310
 A:Experimental source: serogroup B, strain MMD58
 C:Genetics:
 A:Gene: NMB2052

Query Match 76.7% Score 33; DB 2; Length 449;
 Best Local Similarity 87.5%; Pred. No. 32;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IFGSLAFL 9
 Db 135 IFGSLIFL 142

RESULT 12
 S36038 probable olfactory receptor tpcr21 - rat (fragment)
 C:Species: *Rattus norvegicus* (Norway rat)
 C:Accession: S36038
 C:Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 26-Aug-1999
 C:Accession: S58038
 R:Vanderhaeghen, P.; Schurmans, S.; Vassart, G.; Parmentier, M.
 A:Description: Male germ cells from several mammalian species express a specific receptor
 A:Reference number: S37995
 A:Accession: S58038
 A:Status: preliminary
 A: Molecule type: mRNA
 A:Cross-references: EMBL:X89704; NID:902724; PIDN:CAA61851.1; PID:902725
 C:Superfamily: Olfactory receptor OR14

Query Match 76.7% Score 33; DB 2; Length 449;
 Best Local Similarity 85.7%; Pred. No. 19;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FGSLAFL 9
 Db 127 FGSLAFM 133

RESULT 13
 T20547 hypothetical protein F07C6.3 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Accession: T20547
 R:Steward, C.
 A:Description: T20547
 A: Molecule type: DNA
 A:Cross-references: EMBL:269659; PIDN:CAA93484.1; GSPDB:GN000022; CESP:F07C6.3
 A:Experimental source: clone F07C6
 A:Genes: CESP:F07C6.3
 A:Map position: 4
 A:Introns: 14/3; 4/7/3; 68/3; 123/3; 149/3; 179/3
 C:Superfamily: *Caenorhabditis elegans* hypothetical protein F07C6.3

Query Match 74.4% Score 32; DB 2; Length 231;
 Best Local Similarity 62.5%; Pred. No. 27;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

F;2/Modified site: acetylated amino end (Gly) (in mature form) #status predicted
 F;80/Blinding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 74.4%; Score 32; DB 2; Length 323;
 Best Local Similarity 66.7%; Pred. No. 38;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9
 :|||:|||
 Db 179 KVFGELAIL 187

RESULT 14

S60649 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - brine shrimp mitochondrion
 C:Species: mitochondrial Artemia franciscana (brine shrimp)
 C:Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 07-Dec-1999
 C:Accession: S60649
 R: Perez, M.L.; Valverde, J.R.; Batuecas, B.; Amat, F.; Marco, R.; Garesse, R.
 J. Mol. Evol. 38, 156-168, 1999
 A:Title: Speciation in the Artemia genus: mitochondrial DNA analysis of bisexual and parthenogenetic lineages
 A:Reference number: S60649; MUID:94223692
 A:Accession: S60649
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Residues 1-298 <PFR>
 A:Cross-references: EMBL:X69067; NID:9505262; PIDN:CAA48818.1; PID:9578449
 C:Genetics
 C:Superfamily: NADH dehydrogenase (ubiquinone) chain 1
 C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 74.4%; Score 32; DB 2; Length 298;
 Best Local Similarity 62.5%; Pred. No. 35;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IFGSLAFL 9
 :|||:|||
 Db 241 VFGSMSFL 248

RESULT 15

S05035 protein kinase (EC 2.7.1.37), cGMP-dependent, form I-beta - bovine (fragments)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 07-Sep-1990 #sequence_revision 24-Feb-1995 #text_change 04-Feb-2000
 C:Accession: S05035; A32952; A60180
 R: Werner, W.; Flockezi, V.; Hofmann, F.
 FEBS Lett. 251, 191-196, 1989
 A:Title: The cDNA of the two isoforms of bovine cGMP-dependent protein kinase.
 A:Reference number: S05034; MUID:89325663
 A:Accession: S05035
 A:Molecule type: mRNA
 A:Residues 1-293 <WFR>
 A:Cross-references: EMBL:X54289; NID:9213; PIDN:CAA38184.1; PID:9214
 R: Wolfe, L.; Francis, S.H.; Corbin, J.D.
 J. Biol. Chem. 264, 4157-4162, 1989
 A:Title: Properties of a cGMP-dependent monomeric protein kinase from bovine aorta.
 A:Reference number: A32952; MUID:89339489
 A:Accession: A32952
 A:Molecule type: protein
 A:Residues: 'E', 64-75 <W01>
 A:Experimental source: aortic smooth muscle
 A:Note: monomeric form apparently produced by proteolysis during purification
 R: Francis, S.H.; Woodford, T.A.; Wolfe, L.; Corbin, J.D.
 Second Messengers Phosphoproteins 12, 301-310, 1989
 A:Title: Types Ialpha and Ibeta isozymes of cGMP-dependent protein kinase: alternative mRNA
 A:Reference number: A60180
 A:Accession: A60180
 A:Molecule type: protein
 A:Residues: 63-92; 'X', 94; 'X', 219-223; 'X', 225-227; 'X', 230-255; 294-323 <FR>
 C:Superfamily: cGMP-dependent protein kinase; cAMP receptor protein cyclic nucleotide-binding domain homology (fragm)
 C:Keywords: acetylated amino end; alternative splicing; ATP; autophosphorylation; cGMP binding domain homology <CAP1>
 F:118-235-/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology (fragm)
 F:236-293-/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology (fragm)

Result No.	Score	Query	Match	Length	DB	ID	Description	SUMMARIES
1	43	100.0	1254	1	ERBB2_MEASAU	060553 mesocricetus		
2	43	100.0	1255	1	ERBB2_HUMAN	P04626 homo sapien		
3	43	100.0	1257	1	ERBB2_RAT	P06194 rattus norv		
4	34	79.1	298	1	RT03_ACACA	P46754 acanthamoeba		
5	34	79.1	540	1	YFE0_YEAST	P43562 saccharomyces		
6	32	74.4	298	1	N11M_ARTSF	Q37114 artemia salin		
7	32	74.4	502	1	VL2_HPV48	Q80925 human papill		
8	32	74.4	670	1	KGPA_BOVIN	P050516 bos taurus		
9	32	74.4	670	1	KGPA_HUMAN	Q13916 homo sapien		
10	32	74.4	670	1	KGPA_RABBIT	Q77676 orctolagus		
11	32	74.4	686	1	KGPB_BOVIN	P21136 bos taurus		
12	32	74.4	686	1	KGPB_HUMAN	P14619 homo sapien		
13	32	74.4	686	1	KGPB_MOUSE	Q9z020 mus musculus		
14	32	74.4	758	1	YA93_SCHPO	Q09182 schizosaccharomyces pombe		
15	32	74.4	2026	1	YFC5_YEAST	P43571 saccharomyces cerevisiae		
16	31	72.1	2026	1	RHTB_ECOLI	P27847 escherichia coli		
17	31	72.1	240	1	YD37_MYTU	Q10647 mycobacterium tuberculosis		
18	31	72.1	251	1	ALP1_YEAST	P33226 mycobacterium smegmatis		
19	31	72.1	573	1	CICL_RABBIT	P38971 saccharomyces cerevisiae		
20	31	72.1	678	1	CICK_HUMAN	P51804 orctolagus cuniculus		
21	31	72.1	687	1	CICK_RABBIT	P51803 orctolagus cuniculus		
22	31	72.1	687	1	CICK_RAT	Q6f333 rattus norvegicus		
23	31	72.1	687	1	CICK_RAT	P51801 homo sapiens		
24	31	72.1	687	1	CICK_HUMAN	P322504 saccharomyces cerevisiae		
25	31	72.1	956	1	CB31_YEAST	P068285 staphylococcus aureus		
26	30	69.8	120	1	MSCL_STAU	P37471 bacillus subtilis		
27	30	69.8	125	1	DIVM_MOUSE	P97297 mus musculus		
28	30	69.8	184	1	ADML_MOUSE	P75424 mycoplasma pneumoniae		
29	30	69.8	242	1	Y252_MWCNP	P14546 leishmania major		
30	30	69.8	284	1	COX3_LLEITA	P50464 caenorhabditis elegans		
31	30	69.8	348	1	UN97_CAEEL	P24305 comamonas acidovorans		
32	30	69.8	351	1	OM32_COMAC	P39589 bacillus subtilis		
33	30	69.8	399	1	YWBF_BACUS			

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT	1	ERBB2_MEASAU	STANDARD	PRT;	1254 AA.
ID	ERBB2_MEASAU				
AC	Q60553;				
DT	15-DEC-1998 (Rel. 37, Created)				
DT	15-DEC-1998 (Rel. 37, Last sequence update)				
DT	01-OCT-2000 (Rel. 40, Last annotation update)				
DE	"Cloning and activation of the Syrian hamster neu proto-oncogene."				
DF	(P105ERBB2) (NEU PROTO-ONCOGENE)				
GN	ERBB2 OR NEU				
OS	Mesocricetus auratus (Golden hamster).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=NERVE;				
RX	MEDLINE: 94193007				
RA	Nakamura T., Ushijima T., Ishizaka Y., Nagao M., Arai M., Yamazaki Y., Ishikawa T.,				
RT	"Cloning and activation of the Syrian hamster neu proto-oncogene."				
RL	Gene 10:251-255(1994).				
-i-	FUNCTION: ESSENTIAL COMPONENT OF A NEUROGULIN-RECEPTOR COMPLEX, ALTHOUGH NEUROGULINS DO NOT INTERACT WITH IT ALONE. GP30 IS A POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF- α AND AMPHIREGULIN (BY SIMILARITY).				
CC	CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.				
CC	-i- SUBUNIT: HETEROODIMER WITH EACH OF THE OTHER ERBB RECEPTORS (POTENTIAL).				
CC	-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.				
CC	-i- PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES.				
CC	-i- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	-----				
DR	D16295; BAA01801..1; -.				
DR	INTERPRO; IPR000494; -.				
DR	INTERPRO; IPR000719; -.				
DR	INTERPRO; IPR002145; -.				
DR	INTERPRO; IPR002174; -.				
DR	PFAM; PF00757; Furin-like; 1.				
DR	PFAM; PF001030; RecQL domain; 2.				
DR	PFAM; PF00069; Pkinase; 1.				
DR	PROSITE; PS010107; PROTEIN_KINASE_ATP; 1.				
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.				
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.				
KW	Transmembrane; Glycoprotein; Multigene Family; Receptor; Signal;				
KW	Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;				

FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 530 530 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 571 571 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 654 654 I -> V.
 FT VARIANT 655 655 /FTid=VAR_004077.
 FT VARIANT 655 655 I -> V.
 FT CONFLICT 1170 1170 P -> A (IN REF. 2);
 SQ SEQUENCE 1255 AA; 137909 MW; 39E9DDA04DCF962 CRC64;

Query Match 100.0%; Score 43; DB 1; Length 1255;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
 ERBB2_RAT
 ID ERBB2_RAT STANDARD; PRT: 1257 AA.
 AC P06194;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE RECEPTOR PROTEIN-TYROSINE KINASE PRECURSOR (EC 2.7.1.112)
 DE (P155ERB2) (NEU PROTO-ONCOGENE) (EPIDERMAL GROWTH FACTOR RECEPTOR-RELATED PROTEIN).
 DE ERBB2 OR NEU.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Rattus.
 RN [1] SEQUENCE FROM N.A.
 RC TISSUE-NEUROBLASTOMA;
 RX MEDLINE; 86118662.
 RA Bargmann C.I., Hung M.-C., Weinberg R.A.;
 RA "The neu oncogene encodes an epidermal growth factor receptor-related protein.";
 RA Nature 319:226-230(1986).
 RN [2] SEQUENCE OF B52-905 FROM N.A.
 RC TISSUE-SCIATIC NERVE;
 RX MEDLINE; 91225560.
 RA Lai C., Lemke G.;
 RT "An extended family of protein-tyrosine kinase genes differentially expressed in the vertebrate nervous system.";
 RT expressed in the vertebrate nervous system.";
 RL 6:691-704 (1991).
 RN [3] STRUCTURE BY NMR OF 650-668.
 RX MEDLINE; 92155181.
 RA Gullick W.J., Bottomley A.C., Loftus F.J., Doak D.G., Mulvey D., Newman R., Crumpton M.J., Sternberg M.J.E., Campbell I.D.;
 RT "Three dimensional structure of the transmembrane region of the proto-oncogenic and oncogenic forms of the neu protein.";
 RL EMBO J. 11:43-48 (1992).
 CC -1- FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX.
 CC ALTHOUGH NEUREGULINS DO NOT INTERACT WITH IT ALONE, GP30 IS A POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-
 CC ALPHA AND AMPHIREGULIN.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBUNIT: HETEROODIMER WITH EACH OF THE OTHER ERBB RECEPTORS.
 CC THE CONSTITUTIVELY ACTIVATED ONCOGENIC VARIANT FORMS A HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.

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CC DR EMBL; X0362; CAA27059.1; AUT-INT.
 CC DR PIR; A24562; TVRTNU.
 CC DR HSSP; P11362; 1F5I.
 CC DR INTPR0; IPR00494; -.
 CC DR INTPR0; IPR000719; -.
 CC DR INTPR0; IPR001245; -.
 CC DR INTPR0; IPR00214; -.
 CC DR PIR; PF00757; Furin-like; 1.
 CC DR PIR; PF01030; Recp_L-domain; 2.
 CC DR PFAM; PF00069; kinase; 1.
 CC DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 CC DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 CC DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 CC KW Transmembrane; Glycoprotein; Multigene family; Receptor; Signal; Proto-oncogene; Tyrosine-protein kinase; ATP-binding; Phosphorylation; Proto-oncogene; Disease mutation; Potential.
 CC KW ERBB-2 RECEPTOR PROTEIN-TYROSINE KINASE.
 CC EXTRACELLULAR (POTENTIAL).
 CC SIGNAL 1
 CC FT CHAIN 22 1257
 CC FT DOMAIN 22 654
 CC FT TRANSMEM 655 677
 CC FT DOMAIN 678 1257
 CC FT DOMAIN 159 369
 CC FT DOMAIN 473 646
 CC FT DOMAIN 722 989
 CC FT NP-BIND 728 736
 CC FT BINDING 755 755
 CC FT ACT_SITE 847 847
 CC FT VARIANT 661 661
 CC FT MOD_RES 1141 1141
 CC FT MOD_RES 1250 1250
 CC FT CARBOHYD 68 68
 CC FT CARBOHYD 188 188
 CC FT CARBOHYD 260 260
 CC FT CARBOHYD 532 532
 CC FT CARBOHYD 573 573
 CC FT CARBOHYD 631 631
 CC SQ SEQUENCE 1257 AA; 138831 MW; 6129264583011402 CR064;
 CC Query Match 100.0%; Score 43; DB 1; Length 1257;
 CC Best Local Similarity 100.0%; Pred. No. 0.39;
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
 ID RT03_ACACA STANDARD; PRT: 298 AA.
 AC P46754;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE RPS3.
 GN Acanthamoeba castellanii (Ameoba).
 OS Mitochondrion.
 OC Eukaryota; Acanthamoebidae; Acanthamoeba.
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=ATCC 30010 / NEFF;
 RC STRAIN=ATCC 30010 / NEFF;
 RX MEDLINE; 9514725.
 RA Burger G., Planté I., Monergan K.M., Gray M.W.;

RT "The mitochondrial DNA of the amoeboid protozoan, Acanthamoeba castellanii: complete sequence, gene content and genome organization.";
 RT J. Mol. Biol. 245: 522-537 (1995).
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
 CC -1- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.

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DR EMBL; U012386; AA011841.1; -.
 DR INTERPRO; IPR001051; -.
 DR PFAM; PF00189; Ribosomal_S2_C; 1.
 DR PFAM; PF00417; Ribosomal_S3_N; 1.
 DR PROSITE; PS00548; RIBOSOMAL_S3; FALSE_NEG.
 DR Ribosomal protein; Mitochondrion.

KW SEQUENCE 298 AA; 36060 MW; 29415935EE187DE66 CRC64;
 SQ

Query Match 79.1%; Score 34; DB 1; Length 298;
 Best Local Similarity 87.5%; Pred. No. 7.3; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 K1FGSLAF 8
 Db 250 K1FGSLAF 257

RESULT 5
 YPEO_YEAST STANDARD; PRT; 540 AA.
 ID YPEO_YEAST AC
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE PROBABLE METABOLITE TRANSPORT PROTEIN YFL040W.
 GN YFL040W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales; Saccharomyctaceae; Saccharomyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAINS:S288C / AB972;
 RX MEDLINE; 9500299.
 RA Murakami Y., Naito M., Hagiwara H., Shibata T., Ozawa M.,
 RA Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K.,
 RA Yamazaki M., Tasiro H., Eki T.;
 RT "Analysis of the nucleotide sequence of chromosome VI from
 Saccharomyces cerevisiae";
 RP Genet. 10:261-268 (1995).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
 CC -1- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
 CC

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 CC

DR EMBL; D50617; BAA09200.1; -.
 DR EMBL; D44598; BAA08025.1; -.
 DR SGD; SGD1001854; YFL040W.
 DR INTERPRO; IPR001066; -.
 DR PFAM; PF00083; sugar_tr; 1.
 DR PROSITE; PS00216; SUGAR_TRANSPORT_1; FALSE_NEG.
 DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.

KW Hypothetical protein; Repeat; Transport; Transmembrane.
 FT TRANSMEM 30 88
 FT TRANSMEM 68 88
 FT TRANSMEM 102 122
 FT TRANSMEM 127 147
 FT TRANSMEM 159 179
 FT TRANSMEM 188 208
 FT TRANSMEM 276 334
 FT TRANSMEM 314 334
 FT TRANSMEM 342 362
 FT TRANSMEM 386 406
 FT TRANSMEM 429 449
 FT TRANSMEM 456 476
 SEQUENCE 540 AA; 60610 MW; A43B658134C38AE CRC64;

Query Match 79.1%; Score 34; DB 1; Length 540;
 Best Local Similarity 87.5%; Pred. No. 13; Indels 0; Mismatches 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IFGSLAFL 9
 Db 459 IFGSLAFL 466

RESULT 6
 ND1M_ARTSF STANDARD; PRT; 298 AA.
 ID ND1M_ARTSF AC
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE NADH+UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3).
 GN ND1 OR ND-1.
 OS Artemia sanfranciscana (Brine shrimp) (Artemia franciscana).
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;
 OC Artemiidae; Artemia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 942233692.
 RA Perez M.L., Valverde J.R., Batuecas B., Amat F., Marco R., Garesse R.;
 RT "Speciation in the Artemia genus: mitochondrial DNA analysis of bisexual and parthenogenetic brine shrimps.";
 RL J. Mol. Evol. 38:156-168 (1994).
 CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+)+ UBIQUINOL.
 CC -1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.
 CC

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DR INTERPRO; IPR001694; -.
 DR PROSITE; PS00146; NADH1; 1.
 DR PROSITE; PS00667; COMPLEX1_ND1_1; 1.
 DR PROSITE; PS00668; COMPLEX1_ND1_2; 1.
 KW Oxidoreductase; NAD: Ubiquinone; Mitochondrion; Transmembrane.
 SQ SEQUENCE 298 AA; 33763 MW; 07FEP8CD6219E1E CRC64;

Query Match 74.4%; Score 32; DB 1; Length 298;
 Best Local Similarity 62.5%; Pred. No. 19; Indels 0; Mismatches 3; Gaps 0;

Qy 2 IFGSLAFL 9
 Db 241 VFGSMSFL 248

RESULT 7
 VL2_HPV48 STANDARD; PRT; 502 AA.
 ID Q80925; PRT; 502 AA.
 AC 15-JUL-1998 (Rel. 36, Created)
 DR 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE MINOR CAPSID PROTEIN L2.
 GN L2.
 OS Human papillomavirus type 48.
 OC Viruses; dsDNA viruses, no RNA stage; Papovaviridae; Papillomavirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Delius H.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/ DDBJ databases.
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 CC or send an email to license@isb-sib.ch).
 DR EMBL: U31789; AAA79469.1; -.
 DR INTERPRO: IPR000784; -.
 DR PFAM: PF00513; late_protein_L2; 1.
 KW Coat protein; Late protein.
 SEQUENCE 502 AA; 54435 MW; C42DE45A7E73EEB29 CRC64;

Query Match 74.4%; Score 32; DB 1; Length 502;
 Best Local Similarity 75.0%; Pred. No. 32;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KIFGSLAF 8
 DB 43 KIFGSLVY 50

RESULT 8
 KGPA_BOVIN STANDARD; PRT; 670 AA.
 ID KGPA_BOVIN P00516;
 AC 21-JUL-1986 (Rel. 01, Created)
 DR 30-MAY-2000 (Rel. 39, Last sequence update)
 DE CGMP-DEPENDENT PROTEIN KINASE 1, ALPHA ISOZYME (EC 2.7.1.37) (CGK 1
 DE ALPHA) (CGK1-ALPHA).
 GN PRKG1 OR PRKG1A.
 OS Bos taurus (Bovine). Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89325663.
 RA Werner W, Flöckner V, Hofmann F.;
 RT "The cDNA of the two isoforms of bovine cGMP-dependent protein
 kinase.";
 RL FEBS Lett. 251:191-196(1989).
 RN [2]
 RP SEQUENCE OF 1-17; 89-374 AND 407-670.
 RX MEDLINE; 85023307.
 RA Takio K, Wade R.D., Smith S.B., Krebs E.G., Walsh K.A., Titani K.;
 RT "Guanosine cyclic 3',5'-phosphate dependent protein kinase, a
 chimERIC protein homologous with two separate protein families.";
 RL Biochemistry 23:4207-4218(1984).
 RN [3]
 RP SEQUENCE OF 13-104.
 RX MEDLINE; 83213511.
 RA Takio K, Smith S.B., Walsh K.A., Krebs E.G., Titani K.;

"Amino acid sequence around a 'hinge' region and its
 'autophosphorylation' site in bovine Lung cGMP-dependent protein
 kinase.";
 RT J. Biol. Chem. 258:5531-5536(1983).
 RL J. Biol. Chem. 257:727-733(1982).
 RN [4]
 RP SEQUENCE OF 373-409.
 RX MEDLINE; 82098123.
 RA Hashimoto E., Takio K., Krebs E.G.;
 RT "Amino acid sequence at the ATP-binding site of cGMP-dependent
 protein kinase.";
 RL J. Biol. Chem. 257:727-733(1982).
 CC -I- CATALYTIC ACTIVITY: ATP + A PROTEIN = ADP + A PHOSPHOPROTEIN.
 CC -I- ENZYME REGULATION: BINDING OF CGMP TO CGK RESULTS IN ENZYME
 CC ACTIVATION.
 CC -I- SUBUNIT: ANTIPARALLEL HOMODIMER.
 CC -I- ALTERNATIVE PRODUCTS: 2 ISOFORMS: CGK1-ALPHA (SHOWN HERE) AND
 CC CGK1-BETA (P21126); ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -I- MISCELLANEOUS: EXHIBIT A SUBSTRATE SPECIFICITY SIMILAR BUT NOT
 CC IDENTICAL TO THAT OF CAK.
 CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -I- CGMP SUBFAMILY.
 CC -I- SIMILARITY: CONTAINS 2 CYCLIC NUCLEOTIDE-BINDING DOMAINS.
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 CC or send an email to license@isb-sib.ch).
 CC -I-
 DR EMBL; X16086; CAA34214.1; -.
 DR PIR; A00619; ORBOG.
 DR PIR; S05034; S05034.
 DR PIR; S05132; 2CPK.
 DR INTERPRO; IPR000595; -.
 DR INTERPRO; IPR000719; -.
 DR INTERPRO; IPR000961; -.
 DR INTERPRO; IPR002290; -.
 DR INTERPRO; IPR002374; -.
 DR PFAM; PF00027; cNMP_binding; 2.
 DR PFAM; PF00069; kinase; 1.
 DR PFAM; PF00433; kinase_C; 1.
 DR PRINTS; PRO0104; CGMPKINASE.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00889; cNMP_BINDING_1; 2.
 DR PROSITE; PS00889; cNMP_BINDING_2; 2.
 DR PROSITE; PS50042; cNMP_BINDING_3; 2.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW cGMP-binding; Acetylation; Phosphorylation; Acetylation; Phosphorylation.
 FT INIT_MET 0 0
 FT MOD_RES 1 1
 FT DISULFID 42 42
 FT MOD_RES 58 58
 FT DOMAIN 1 101
 FT NP_BIND 102 219
 FT NP_BIND 220 340
 FT DOMAIN 359 618
 FT NP_BIND 365 373
 FT BINDING 389 389
 FT ACT_SITE 483 483
 SQ SEQUENCE 670 AA; 76287 MW; A8E37ACFCB8A7557D CRC64;

Query Match 74.4%; Score 32; DB 1; Length 670;
 Best Local Similarity 66.7%; Pred. No. 42;
 Matches 6; Conservative 1; Mismatches 2; Indels 0;
 Gaps 0;
 QY 1 KIFGSLFL 9
 DB 163 KVFGELAIL 171

RESULT: 9

KGPA_HUMAN STANDARD; PRT; 670 AA.

AC Q13976; (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE CGMP-DEPENDENT PROTEIN KINASE 1, ALPHA ISOZYME (EC 2.7.1.37) (CGK 1.

DE ALPHA) (CGK1-ALPHA).

GN PRKG1 OR PRK1A.

OS Homo sapiens (Human).

RA Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Homo; Mammalia; Eutheria; Primates; Catarhini; Hominoidea; Homo.

[1]

RP SEQUENCE FROM N.A.

RC TISSUE-LUNG;

RA MEDLINE; 96188981.

RA Suga S., Ogawa Y., Nakagawa O., Harada M., Chun T., Tamura N., Itoh H., Ogawa Y., Nakao K.; "cDNA cloning and gene expression of human type Ialpha cGMP-dependent protein kinase," J. Hypertension 27:552-557(1996).

[2]

RP SEQUENCE FROM N.A.

RA Orstavik S., Natarajan V., Tasken K., Juhnsen T., Sandberg M.; "Characterization of the human gene encoding the type I alpha and type I beta cGMP-dependent protein kinase (PRKG1)."; Genomics 42:311-318(1997).

RL 97336057.

RA MEDLINE; 97336057.

RA MEDLINE; 96188981.

RA Suga S., Ogawa Y., Nakagawa O., Nakao K.; "cDNA cloning and gene expression of human type Ialpha cGMP-dependent protein kinase," J. Hypertension 27:552-557(1996).

CC -1- ENZYME REGULATION: BINDING OF CGMP TO CGK RESULTS IN ENZYME ACTIVATION (BY SIMILARITY).

CC -1- SUBUNIT: ANTI-PARALLEL HOMODIMER (BY SIMILARITY).

CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CGK1-ALPHA (SHOWN HERE) AND CGK1-BETA (P14619); ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- MISCELLANEOUS: EXHIBIT A SUBSTRATE SPECIFICITY SIMILAR BUT NOT IDENTICAL TO THAT OF CAK (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -1- SIMILARITY: CONTAINS 2 CYCLIC NUCLEOTIDE-BINDING DOMAINS.

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CC DR EMBL; 292867; CAB07436.1; JOINED.

CC DR EMBL; 292869; CAB07436.1; JOINED.

CC DR EMBL; 292870; CAB07436.1; JOINED.

CC DR EMBL; 292871; CAB07436.1; JOINED.

CC DR EMBL; 292872; CAB07436.1; JOINED.

CC DR EMBL; 292873; CAB07436.1; JOINED.

CC DR EMBL; 292874; CAB07436.1; JOINED.

CC DR EMBL; 292875; CAB07436.1; JOINED.

CC DR EMBL; 292876; CAB07436.1; JOINED.

CC DR EMBL; 292877; CAB07436.1; JOINED.

CC DR EMBL; 292878; CAB07436.1; JOINED.

CC DR EMBL; 292879; CAB07436.1; JOINED.

CC DR EMBL; 292880; CAB07436.1; JOINED.

CC DR EMBL; 292881; CAB07436.1; JOINED.

CC DR EMBL; 292882; CAB07436.1; JOINED.

CC DR EMBL; 292883; CAB07436.1; JOINED.

CC DR EMBL; 292884; CAB07436.1; JOINED.

CC DR EMBL; 292885; CAB07436.1; JOINED.

CC DR EMBL; 104566; BA08297.1; JOINED.

CC DR EMBL; 176894; -.

DR INTERPRO; IPR000595; -.

DR INTERPRO; IPR000719; -.

DR INTERPRO; IPR002373; -.

DR INTERPRO; IPR002374; -.

DR INTERPRO; IPR002375; -.

DR INTERPRO; IPR002376; -.

DR PEPTIDE; PE00027; CNMP-binding; 2.

DR PEPTIDE; PE00069; Pkinase; 1.

DR PEPTIDE; PE00433; Pkinase_C; 1.

DR PRINTS; PRO0103; CAMPKINASE.

DR PRINTS; PRO0104; CGMPKINASE.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00112; CNMP_BINDING_1; 2.

DR PROSITE; PS00889; CNMP_BINDING_2; 2.

DR PROSITE; PS50042; CNMP_BINDING_3; 2.

KW Transferase; Serine/threonine-protein kinase; ATP-binding; Acetylation; Phosphorylation; Alternative splicing.

KW CGMP-binding; Acetylation; Phosphorylation; Alternative splicing.

KW ACETYLATION (BY SIMILARITY).

KW INTERCHAIN (WITH DIMER) (BY SIMILARITY).

KW PHOSPHORYLATION (AUTO) (BY SIMILARITY).

KW DIMERIZATION (BY SIMILARITY).

FT INT_MET 0 0

FT MOD_RES 1 1

FT DISULFID 42 42

FT MOD_RES 58 58

FT DOMAIN 1 101

FT NP_BIND 102 219

FT NP_BIND 220 340

FT DOMAIN 359 618

FT NP_BIND 365 373

FT BINDING 389 389

FT ACT-SITE 483 483

SQ SEQUENCE 670 AA; 76233 MW; 663C4B496F983270 CRC64;

Query Match 74.4%; Score 32; DB 1; Length 670;

Best Local Similarity 66.7%; Pred. No. 42;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9

Db 163 KVFGELAIL 171

RESULT: 10

KGPA_RABBIT STANDARD; PRT; 670 AA.

ID KGPA_RABBIT

AC 077676;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE CGMP-DEPENDENT PROTEIN KINASE 1, ALPHA ISOZYME (EC 2.7.1.37) (CGK 1

DE ALPHA) (CGK1-ALPHA).

DE PRKG1.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagidae.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NEW ZEALAND WHITE; TISSUE=HEART;

CC Kumar R., Joyner R. W., Lincoln T. M.;

CC RT cDNA cloning and analysis of expression of cGMP-dependent protein kinase in rabbit heart.;

CC RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN = ADP + A PHOSPHOPROTEIN.

CC -1- ENZYME REGULATION: BINDING OF CGMP TO CGK RESULTS IN ENZYME ACTIVATION (BY SIMILARITY).

CC -1- SUBUNIT: ANTI-PARALLEL HOMODIMER (BY SIMILARITY).

CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CGK1-ALPHA (SHOWN HERE) AND CGK1-BETA; ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- MISCELLANEOUS: EXHIBIT A SUBSTRATE SPECIFICITY SIMILAR BUT NOT IDENTICAL TO THAT OF CAK (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -1- SIMILARITY: CONTAINS 2 CYCLIC NUCLEOTIDE-BINDING DOMAINS.

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CC DR EMBL; 292867; CAB07436.1; JOINED.

CC DR EMBL; 292869; CAB07436.1; JOINED.

CC DR EMBL; 292870; CAB07436.1; JOINED.

CC DR EMBL; 292871; CAB07436.1; JOINED.

CC DR EMBL; 292872; CAB07436.1; JOINED.

CC DR EMBL; 292873; CAB07436.1; JOINED.

CC DR EMBL; 292874; CAB07436.1; JOINED.

CC DR EMBL; 292875; CAB07436.1; JOINED.

CC DR EMBL; 292876; CAB07436.1; JOINED.

CC DR EMBL; 292877; CAB07436.1; JOINED.

CC DR EMBL; 292878; CAB07436.1; JOINED.

CC DR EMBL; 292879; CAB07436.1; JOINED.

CC DR EMBL; 292880; CAB07436.1; JOINED.

CC DR EMBL; 292881; CAB07436.1; JOINED.

CC DR EMBL; 292882; CAB07436.1; JOINED.

CC DR EMBL; 292883; CAB07436.1; JOINED.

CC DR EMBL; 292884; CAB07436.1; JOINED.

CC DR EMBL; 292885; CAB07436.1; JOINED.

CC DR EMBL; 104566; BA08297.1; JOINED.

CC DR EMBL; 176894; -.

DR INTERPRO; IPR000595; -.

DR INTERPRO; IPR000719; -.

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 CC

EMBL: AF076969; AAC31192.1; -.
 DR INTRPRO; IPR002373; -.
 DR INTRPRO; IPR002374; -.
 DR PFAM; PF00027; CNMP_binding; 2.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00888; CNMP_BINDING_1; 2.
 DR PROSITE; PS00889; CNMP_BINDING_2; 2.
 DR PROSITE; PS50042; CNMP_BINDING_3; 2.
 DR TRANSFERASE; Serine/threonine-protein kinase; ATP-binding;
 KW CGMP-binding; Acetylation; Phosphorylation; Alternative splicing.
 FT INIT_MET 0 BY SIMILARITY.
 FT MOD_RES 1 ACETYLATION (BY SIMILARITY).
 FT DISULFID 1 INTERCHAIN (WITH DIMER) (BY SIMILARITY).
 FT MOD_RES 42 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT DOMAIN 58 DIMERIZATION (BY SIMILARITY).
 FT DOMAIN 1 101 CGMP 1.
 FT NP_BIND 102 219 CGMP 2.
 FT NP_BIND 220 340 PROTEIN_KINASE.
 FT DOMAIN 359 618 ATP (BY SIMILARITY).
 FT NP_BIND 365 373 ATP (BY SIMILARITY).
 FT BINDING 389 389 BY SIMILARITY.
 FT ACT_SITE 483 483 BY SIMILARITY.
 FT VARIANT 557 557 F->S.
 SQ SEQUENCE 670 AA; 76322 MW; CPE1D7D939E1C423 CRC64;

Query Match 74.4%; Score 32; DB 1; Length 670;
 Best Local Similarity 66.7%; Pred. No. 42;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9
 Db 163 KVFGELAIL 171

RESULT 11
 KGPB_BOVIN STANDARD; PRT; 686 AA.
 ID P21136; STANDARD; PRT; 686 AA.
 AC P21136; KIFGSLAFL 9.
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CGMP-DEPENDENT PROTEIN KINASE 1, BETA ISOZYME (EC 2.7.1.37) (CGK 1
 DE PRKG1, OR PRKG1B, OR PRKG1B).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinac; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RX MEDLINE; 9725567.

RA Ruth P., Pfeifer A., Kamm S., Klatt P., Dostmann W.R., Hofmann F.;
 RT "Identification of the amino acid sequences responsible for high
 affinity activation of CGMP kinase Ialpha.";
 RL J. Biol. Chem. 272:10522-10528 (1997).
 RN [2]
 RP SEQUENCE OF 1-293 FROM N.A.
 RC TISSUE=TRACHEA SMOOTH MUSCLE;
 RX MEDLINE; 89325663.
 RA Werner W., Flockezi V., Hofmann F.;
 RT "The cDNA of the two isoforms of bovine cGMP-dependent protein
 kinase.";
 RL FEBS Lett. 251:191-196 (1989).
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN = ADP + A PHOSPHOPROTEIN.
 CC -1- ENZYME REGULATION: BINDING OF CGMP TO CGK RESULTS IN ENZYME
 ACTIVATION.
 CC -1- SUBUNIT: ANTIPARALLEL HOMODIMER.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CGK1-ALPHA (P00516) AND
 CC CGK1-BETA (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- MISCELLANEOUS: EXHIBIT A SUBSTRATE SPECIFICITY SIMILAR BUT NOT
 CC IDENTICAL TO THAT OF CAK.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CGMP SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 2 CYCLIC NUCLEOTIDE-BINDING DOMAINS.
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 CC

EMBL: Y08961; CAA381184.1; -.
 DR EMBL: X54289; CAA381184.1; -.
 DR PIR: S05035; S05035.
 DR HSPP; P05132; 2CPK.
 DR INTERPRO; IPR000595; -.
 DR INTERPRO; IPR000719; -.
 DR INTERPRO; IPR000961; -.
 DR INTERPRO; IPR002290; -.
 DR INTERPRO; IPR002374; -.
 DR PFAM; PF00027; CNMP_binding; 2.
 DR PFAM; PF00069; pkinase; 1.
 DR PFAM; PF00433; pkinase_C; 1.
 DR PRINS; PR00104; CGMPKINASE.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00888; CNMP_BINDING_1; 2.
 DR PROSITE; PS00889; CNMP_BINDING_2; 2.
 DR PROSITE; PS50042; CNMP_BINDING_3; 2.
 DR TRANSFERASE; Serine/threonine-protein kinase; ATP-binding;
 KW CGMP-binding; Acetylation; Phosphorylation; Alternative splicing.
 FT INIT_MET 0 BY SIMILARITY.
 FT MOD_RES 1 ACETYLATION (BY SIMILARITY).
 FT DISULFID 42 INTERCHAIN (WITH DIMER) (BY SIMILARITY).
 FT MOD_RES 58 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT DOMAIN 1 101 CGMP 1.
 FT NP_BIND 102 219 CGMP 2.
 FT DOMAIN 220 340 PROTEIN_KINASE.
 FT DOMAIN 359 618 ATP (BY SIMILARITY).
 FT NP_BIND 365 373 ATP (BY SIMILARITY).
 FT BINDING 389 389 BY SIMILARITY.
 FT ACT_SITE 483 483 BY SIMILARITY.
 FT VARIANT 557 557 F->S.
 SQ SEQUENCE 670 AA; 76322 MW; CPE1D7D939E1C423 CRC64;

Query Match 74.4%; Score 32; DB 1; Length 686;
 Best Local Similarity 66.7%; Pred. No. 43;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9
 Db 179 KVFGELAIL 187

RESULT 12
 KGPB_HUMAN
 AC P21136; KIFGSLAFL 9.
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CGMP-DEPENDENT PROTEIN KINASE 1, BETA ISOZYME (EC 2.7.1.37) (CGK 1
 DE PRKG1, OR PRKG1B, OR PRKG1B).
 OS Bovidae; Bovinac; Bos.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinac; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RX MEDLINE; 9725567.

ID	KGPB_HUMAN	STANDARD;	PRT;	686 AA.	
AC	P14619;				
DT	01-APR-1990 (Rel. 14, Created)				
DT	01-APR-1990 (Rel. 14, Last sequence update)				
DT	30-MAY-2000 (Rel. 39, Last annotation update)				
DE	CGMP-DEPENDENT PROTEIN KINASE 1, BETA ISOZYME (EC 2.7.1.37) (CGK 1)				
DE	CGK1-BETA.				
GN	PRKG1 OR PRKGR1B OR PRKG1B.				
OS	<i>Homosapiens</i> (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
RN	[1]				
RC	SEQUENCE FROM N.A.				
RC	TISSUE=PLACENTA;				
RX	MEDLINE; 9005998.				
RA	Sandberg M., Natrajan V., Ronander I., Kaldern D., Walter U., Lohmann S.M., Janssen T.				
RT	Molecular cloning and predicted full-length amino acid sequence of the type I beta isozyme of cGMP-dependent protein kinase from human placenta. Tissue distribution and developmental changes in rat.				
RT	"				
RL	FEBS Lett. 255:321-329(1985).				
RN	[2]				
RP	REVISIONS.				
RA	Sandberg M.;				
RA	Submitted (OCT-1989) to the EMBL/Genbank/DDBJ databases.				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 97336057.				
RA	Orstavik S., Natrajan V., Tasken K., Janssen T., Sandberg M.;				
RT	Characterization of the human gene encoding the type I alpha and type I beta cGMP-dependent protein kinase (PRKG1).;				
RL	Genomics 42:311-318(1997).				
CC	-I- CATALYTIC ACTIVITY: ATP + A PROTEIN = ADP + A PHOSPHOPROTEIN.				
CC	-I- ENZYME REGULATION: BINDING OF CGMP TO CGK RESULTS IN ENZYME ACTIVATION.				
CC	-I- SUBUNIT: ANTI-PARALLEL HOMODIMER.				
CC	-I- ALTERNATIVE PRODUCTS: 2 ISOFORMS, CGK1-ALPHA (Q13976) AND CGK1-BETA (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPlicing.				
CC	-I- MISCELLANEOUS: EXHIBIT A SUBSTRATE SPECIFICITY SIMILAR BUT NOT IDENTICAL TO THAT OF CAK.				
CC	-I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.				
CC	-I- CGMP SUBFAMILY.				
CC	-I- SIMILARITY: CONTAINS 2 CYCLIC NUCLEOTIDE-BINDING DOMAINS.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and thus statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL: Y07512; CAB68810.1; -				
DR	EMBL: 292868; CAB07437.1; -				
DR	EMBL: 292869; CAB07437.1; JOINED.				
DR	EMBL: 292870; CAB07437.1; JOINED.				
DR	EMBL: 292871; CAB07437.1; JOINED.				
DR	EMBL: 292872; CAB07437.1; JOINED.				
DR	EMBL: 292873; CAB07437.1; JOINED.				
DR	EMBL: 292874; CAB07437.1; JOINED.				
DR	EMBL: 292875; CAB07437.1; JOINED.				
DR	EMBL: 292876; CAB07437.1; JOINED.				
DR	EMBL: 292877; CAB07437.1; JOINED.				
DR	EMBL: 292878; CAB07437.1; JOINED.				
DR	EMBL: 292879; CAB07437.1; JOINED.				
DR	EMBL: 292880; CAB07437.1; JOINED.				
DR	EMBL: 292881; CAB07437.1; JOINED.				
DR	EMBL: 292882; CAB07437.1; JOINED.				
DR	EMBL: 292883; CAB07437.1; JOINED.				
DR	EMBL: 292884; CAB07437.1; JOINED.				
DR	EMBL: 292885; CAB07437.1; JOINED.				
DR	PIR: S05702; S05702.				
DR	HSSP; P05132; 2CFK.				
DR	MIM: 176894; -				
DR	INTERPRO; IPR000595; -				
DR	INTERPRO; IPR000719; -				
DR	INTERPRO; IPR000961; -				
DR	INTERPRO; IPR002390; -				
DR	INTERPRO; IPR002374; -				
DR	PFAM; PF00027; CNMP_BINDING; 2.				
DR	PFAM; PF00069; kinase; 1.				
DR	PFAM; PF00433; kinase; C; 1.				
DR	PRINTS; PRO0104; CGMPKINASE.				
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.				
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.				
DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.				
DR	PROSITE; PS00888; CNMP_BINDING; 2.				
DR	PROSITE; PS00042; CNMP_BINDING_3; 2.				
KW	Transferase; Serine/threonine-protein kinase; ATP-binding;				
KW	CGMP-binding; Alternative splicing.				
FT	NP_BIND 118 235 CGMP 1 (BY SIMILARITY).				
FT	NP_BIND 236 427 CGMP 2 (BY SIMILARITY).				
FT	DOMAIN 375 634 PROTEIN KINASE.				
FT	NP_BIND 381 389 ATP (BY SIMILARITY).				
FT	BLINDING 405 405 ATP (BY SIMILARITY).				
FT	ACT_SITE 499 499 ATP (BY SIMILARITY).				
SQ	SEQUENCE 686 AA; A097041AB284F1E6 CRC64;				
Query	1 KIFGSLAFL 9				
Match	1:1 1:1 1:1				
Best Local Similarity	74.4%				
Matches	6; Conservative				
Pred.	66.7%; No. 43;				
Mismatches	2;				
Indels	0;				
Gaps	0;				
Db	179 KVFGELAIL 187				
RESULT	13				
KGPB_MOUSE	STANDARD;				
ID	KGPB_MOUSE				
AC	O92020;				
DT	30-MAY-2000 (Rel. 39, Created)				
DT	30-MAY-2000 (Rel. 39, Last sequence update)				
DT	30-MAY-2000 (Rel. 39, Last annotation update)				
DE	CGMP-DEPENDENT PROTEIN KINASE 1, BETA ISOZYME (EC 2.7.1.37) (CGK 1 BETA) (CGK1-BETA).				
DE	PRKG1 OR PRKGR1B OR PRKG1B.				
GN	Mus musculus (Mouse)				
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	RESTRAINC57BL/6; TISSUE=BRAIN;				
RX	MEDLINE; 99185034.				
RA	Collins S.P., Uhler M.D.;				
RT	Cyclic AMP + cyclic GMP-dependent protein kinases differ in their regulation of cyclic AMP response element-dependent gene transcription.				
RT	transcription.				
RL	J. Biol. Chem. 274:8391-8404 (1999).				
CC	-I- CATALYTIC ACTIVITY: ATP + A PROTEIN = ADP + A PHOSPHOPROTEIN.				
CC	-I- ENZYME REGULATION: BINDING OF CGK RESULTS IN ENZYME ACTIVATION (BY SIMILARITY).				
CC	-I- SUBUNIT: ANTI-PARALLEL HOMODIMER (BY SIMILARITY).				
CC	-I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CGK1-ALPHA AND CGK1-BETA (SHOWN HERE); EXHIBIT A SUBSTRATE SPECIFICITY SIMILAR BUT NOT IDENTICAL TO THAT OF CAK (BY SIMILARITY).				
CC	-I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.				
CC	-I- SIMILARITY: CONTAINS 2 CYCLIC NUCLEOTIDE-BINDING DOMAINS.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and thus statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL: Y07512; CAB68810.1; -				
DR	EMBL: 292868; CAB07437.1; -				
DR	EMBL: 292869; CAB07437.1; JOINED.				
DR	EMBL: 292870; CAB07437.1; JOINED.				
DR	EMBL: 292871; CAB07437.1; JOINED.				
DR	EMBL: 292872; CAB07437.1; JOINED.				
DR	EMBL: 292873; CAB07437.1; JOINED.				
DR	EMBL: 292874; CAB07437.1; JOINED.				
DR	EMBL: 292875; CAB07437.1; JOINED.				
DR	EMBL: 292876; CAB07437.1; JOINED.				
DR	EMBL: 292877; CAB07437.1; JOINED.				
DR	EMBL: 292878; CAB07437.1; JOINED.				
DR	EMBL: 292879; CAB07437.1; JOINED.				
DR	EMBL: 292880; CAB07437.1; JOINED.				
DR	EMBL: 292881; CAB07437.1; JOINED.				
DR	EMBL: 292882; CAB07437.1; JOINED.				
DR	EMBL: 292883; CAB07437.1; JOINED.				
DR	EMBL: 292884; CAB07437.1; JOINED.				
DR	EMBL: 292885; CAB07437.1; JOINED.				
DR	PIR: S05702; S05702.				
DR	HSSP; P05132; 2CFK.				
CC	-I- SIMILARITY: CONTAINS 2 CYCLIC NUCLEOTIDE-BINDING DOMAINS.				
CC	-----				
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CC	-----				

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EMBL: AF084541; AAC160441; .

 MGI: MGI:108174; PRKG1.

 INTERPRO: IPR000595; .

 INTERPRO: IPR000719; .

 INTERPRO: IPR000961; .

 INTERPRO: IPR001245; .

 INTERPRO: IPR002290; .

 INTERPRO: IPR002373; .

 INTERPRO: IPR002374; .

 PFAM: PF00027; CNMP_binding; 2.

 PFAM: PF00069; kinase; 1.

 PFAM: PF00433; kinase_c; 1.

 PFAM: PF00103; CAMPKINASE.

 PRINTS: PRO0104; CGMPKINASE.

 PRINTS: PRO0109; TYRKINASE.

 PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.

 PROSITE: PS00108; PROTEIN_KINASE_ST; 1.

 PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.

 PROSITE: PS00888; CNMP_BINDING_1; 2.

 PROSITE: PS00899; CNMP_BINDING_2; 2.

 PROSITE: PS50042; CNMP_BINDING_3; 2.

 TRANSFERASE: Serine/threonine-protein kinase; ATP-binding; CGMP-binding; Alternative splicing; CGMP_1 (BY SIMILARITY).

 NP_BIND 118 235 CGMP_2 (BY SIMILARITY).

 NP_BIND 236 427 PROTEIN_KINASE.

 DOMAIN 375 634 ATP (BY SIMILARITY).

 NP_BIND 389 405 ATP (BY SIMILARITY).

 BINDING 405 405 BY SIMILARITY.

 ACT_SITE 499 499 BY SIMILARITY.

 SEQUENCE 686 AA: 77789 MW: A0281F553093616 CRC64; .

Query Match 74 4%; Score 32; DB 1; Length 686;

Best Local Similarity 66 7%; Pred. No. 43; Gaps 0;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Y 1 KIFGSLAF 9

Y 1:1:1:1:1 179 KVFGELAIL 187

RESULT 14

 I93_SCHPO STANDARD; PRT; 758 AA.

 D YA93_SCHPO

 D 009782; PRT; 758 AA.

 C 01-NOV-1995 (Rel. 32, Created)

 C 01-NOV-1995 (Rel. 32, Last sequence update)

 C 01-NOV-1995 (Rel. 32, Last annotation update)

 C HYPOTHETICAL 85.7 KDA PROTEIN C13G6_03 IN CHROMOSOME I.

 C SPAC13G6_03.

 C Schizosaccharomyces pombe (Fission Yeast).

 C Eukaryote; Fungi; Ascomycota; Schizosaccharomyctales;

 C Schizosaccharomyctaceae; Schizosaccharomyces.

 C [1]

 C SEQUENCE FROM N.A.

 C STRAIN=972;

 C Odell C.; Bowman S.; Barrell B.G.; Ralandream M.A.; Walsh S.V.;

 C RA Submitted (Sep-1995) to the EMBL/GenBank/DDJB databases.

 C RL - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

 C IC - SIMILARITY: TO YEAST HRC330.

 C

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 C entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC	DR	EMBL; 254308; CAA81096.1; -.
	KW	Hypothetical protein; Transmembrane.
	FT	TRANSMEM 4 24 POTENTIAL.
	FT	TRANSMEM 3.09 3.29 POTENTIAL.
	FT	TRANSMEM 4.05 4.25 POTENTIAL.
	FT	TRANSMEM 4.31 4.51 POTENTIAL.
	FT	TRANSMEM 5.10 5.30 POTENTIAL.
	FT	TRANSMEM 5.33 5.53 POTENTIAL.
	FT	TRANSMEM 5.61 5.81 POTENTIAL.
	FT	TRANSMEM 5.98 6.18 POTENTIAL.
	FT	TRANSMEM 6.67 6.87 POTENTIAL.
	FT	TRANSMEM 6.98 7.18 POTENTIAL.
	FT	TRANSMEM 7.33 7.53 POTENTIAL.
SQ	SEQUENCE	758 AA; 85665 MW; F0FE169B570ACC57 CRC64;
		Query Match 74.4%; Score 32; DB 1; Length 758;
	Best Local Similarity 66.7%;	Pred. NO. 47;
	Matches 6;	Mismatches 1; Indels 0; Gaps 0;
Qy	1	K1FGSLAFL 9
Db	12	Q1FQSTFL 20
	RESULT 15	
	YFC5_YEAST	
	ID YFC5_YEAST	STANDARD;
	AC P43571;	PRP; 1029 AA.
	DT 01-NOV-1995 (Rel. 32, Created)	
	DT 01-NOV-1995 (Rel. 32, Last sequence update)	
	DT 01-NOV-1995 (Rel. 32, Last annotation update)	
	DE HYPOTHETICAL 117.8 KDA PROTEIN IN STE-FRS2 INTERGENIC REGION.	
	GN YFL225C.	
	OS Saccharomyces cerevisiae (Baker's yeast).	
	OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycales;	
	OC Saccharomyctaceae; Saccharomyces; Saccharomyces.	
	RN [1]	
	RP SEQUENCE FROM N.A.	
	RA STRAIN=S288C / AB972;	
	RX MEDLINE; 95400292.	
	RA Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,	
	RA Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K.,	
	RA Yamazaki M., Tashiro H., Eki T.	
	RT "Analysis of the nucleotide sequence of chromosome VI from	
	RT Saccharomyces cerevisiae".	
	RL Nat Genet; 10:261-268(1995);	
	-1 - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).	
	CC SGD; S0001869; BSTL.	
	KW Hypothetical protein; Transmembrane.	
	FT TRANSMEM 57 77 POTENTIAL.	
	FT TRANSMEM 80.4 824 POTENTIAL.	
	FT TRANSMEM 87.2 892 POTENTIAL.	
	FT TRANSMEM 92.0 940 POTENTIAL.	
	FT TRANSMEM 95.7 977 POTENTIAL.	
	FT TRANSMEM 98.5 1005 POTENTIAL.	
SQ	SEQUENCE	1029 AA; 117754 MW; 10B7B212E5AD6B6 CRC64;
	Query Match 74.4%; Score 32; DB 1; Length 1029;	
	Best Local Similarity 77.0%;	Pred. NO. 64;
	Matches 7;	Mismatches 2; Indels 0; Gaps 0;

Qy 1 K1FGSLAFL 9
111111111
Db 826 K1FGSLEIL 834

Search completed: November 14, 2000, 11:56:11
Job time: 89 sec

Database :	SPTREMBL_14.*			
1:	sp_archaea:*			
2:	sp_bacteria:*			
3:	sp_fungi:*			
4:	sp_human:*			
5:	sp_invertebrate:*			
6:	sp_mammal:*			
7:	sp_mhc:*			
8:	sp_organelle:*			
9:	sp_phage:*			
10:	sp_plant:*			
11:	sp_rabbit:*			
12:	sp_virus:*			
13:	sp_vertebrate:*			
14:	sp_unclassified:*			

Listings first 45 summaries

Run on:	November 14, 2000, 11:54:42 ;	Search time 18.18 Seconds
(without alignments)		
46.225 Million cell updates/sec		
Title:	US-09-277-074-10	
Perfect score:	43	
Sequence:	1 KIFGSLAFL 9	
Scoring table:	BLOSUM62	
Gapop 10.0 , Gapext 0.5		
Searched:	297973 seqs, 93374136 residues	
Total number of hits satisfying chosen parameters:	297973	
Minimum DB seq length: 0		
Maximum DB seq length: 2000000000		
Post-processing: Minimum Match 0%		
Maximum Match 100%		
Listing first 45 summaries		

023402 arabidopsis	20	31	72.1	475 10 O23402
09u25 caenorhabdi	21	31	72.1	505 5 O9u25
09v812 drosophila	22	31	72.1	552 5 O9v812
09w10 drosophila	23	31	72.1	589 5 O9w10
09s1x8 arabidopsis	24	31	72.1	616 10 O9s1x8
09wub7 mus musculus	25	31	72.1	687 11 O9wub7
09tvu8 xenopus lae	26	31	72.1	689 13 O9tvu8
09tvu8 caenorhabdi	27	31	72.1	962 5 O9tvu8
044405 caenorhabdi	28	31	72.1	965 5 O44405
044405 caenorhabdi	29	31	72.1	1142 5 O22528
076737 dictyostell	30	31	72.1	3848 5 O76737
P74440 synchocystis	31	31	72.1	4199 2 P74440
09v196 drosophila	32	30.5	70.9	2307 5 09v196
P97453 mus musculus	33	30	69.8	3351 5 P97453
P97297 mus musculus	34	30	69.8	51 8 020187
P9x107 thermotoga	35	30	69.8	77 2 P9x107
050883 borellia hu	36	30	69.8	80 2 050883
P74900 thermus aqu	37	30	69.8	99 2 P74900
P07930 saecharmyc	38	30	69.8	161 3 P07930
P97366 synchocystis	39	30	69.8	184 11 P97366
034935 leishmania	40	30	69.8	184 11 P97297
035993 trypanosoma	41	30	69.8	222 2 P73366
044697 caenorhabdi	42	30	69.8	287 8 P34935
045710 caenorhabdi	43	30	69.8	288 8 Q35993
045710 caenorhabdi	44	30	69.8	336 5 Q44697
045710 caenorhabdi	45	30	69.8	338 5 Q45710

ALIGNMENTS

RESULT	1			
ID	018735	PRELIMINARY;		PRT; 1259 AA.
AC	018735;			
DT	01-JAN-1998 (TREMBLel.	05, Created)		
DT	01-MAY-1998 (TREMBLel.	05, Last sequence update)		
DT	01-MAY-2000 (TREMBLel.	13, Last annotation update)		
DE	ERBB-2.			
OS	Canis familiaris (Dog)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Yokota H.;			
DR	Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.			
DR	EMBL; AB008451; BAN23127.1; -			
DR	HSSP; P00523; 2PTK.			
DR	INTERPRO; IPR000494; -			
DR	INTERPRO; IPR000719; -			
DR	INTERPRO; IPR001245; -			
DR	INTERPRO; IPR002048; -			
DR	INTERPRO; IPR002174; -			
DR	PFAM; PF00069; Pkinase; 1.			
DR	PFAM; PF00757; Furin-like; 1.			
DR	PFAM; PF01030; Reccep_L_domain; 2.			
DR	PROSITE; PS00018; EF_HAND; UNKNOWN_1.			
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.			
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.			
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.			
SQ	SEQUENCE 1259 AA; 137989 MW; E37364D4 9C4ACD46 CRC64;			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	43	100.0	1259	6 Q9XTU7	041835 canis familiaris
2	36	83.7	356	5 O44592	044592 caenorhabdi
3	36	83.7	502	1 O74002	074002 pyrococcus
4	33	76.7	120	5 O20695	020695 caenorhabdi
5	33	76.7	1760	5 Q9VLT3	Q9VLT3 drosophila
6	32	74.4	157	11 Q63595	Q63595 rattus norvegicus
7	32	74.4	221	11 Q9Z230	Q9Z230 rattus norvegicus
8	32	74.4	223	11 Q9ZLY5	Q9ZLY5 mus musculus
9	32	74.4	231	5 Q19158	Q19158 caenorhabdi
10	32	74.4	454	5 Q9XLU7	Q9XLU7 caenorhabdi
11	32	74.4	500	5 Q9VKC2	Q9VKC2 drosophila
12	31	72.1	50	10 Q43282	Q43282 arabidopsis
13	31	72.1	149	12 Q9YVVS	Q9YVVS melanoplus
14	31	72.1	232	1 Q26659	Q26659 methanobacter
15	31	72.1	264	2 Q9Z980	Q9Z980 chlamydia p
16	31	72.1	326	2 Q9XU07	Q9XU07 thermotoga
17	31	72.1	335	5 Q17809	Q17809 caenorhabdi
18	31	72.1	343	5 Q9UAX3	Q9UAX3 caenorhabdi
19	31	72.1	350	5 P91506	P91506 caenorhabdi

Best Local Similarity

9;

Matches

0;

Mismatches

0;

Indels

0;

Gaps

0;

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044592;	PRELIMINARY;	PRT;	356 AA.	
AC				
DT	01-JUN-1998 (TREMBLrel. 06, Created)			
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)			
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)			
DE	F48G7_1. PROTEIN.			
GN	F48G7_1.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoides;			
OC	Rhabditidae; Peloderaiae; Caenorhabditis.			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=BRISTOL N2;			
RC	RE			
RA	Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Berks M.,			
RA	Craxton M., Dear S., Durbin R., Favello A., Fulton L.,			
RA	Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,			
RA	Jones M., Kershaw J., Kirsten J., Laird N., Latreille P.,			
RA	Lightning J., Lloyd C., McMurtore B., O'Callaghan M.,			
RA	Parsons J., Percy C., Riffen L., Roopra A., Saunders D., Shawken R.,			
RA	Smaulon N., Smith A., Sonnhammer E., Staden R., Sulston J.,			
RA	Thiberry-Mieg J., Thomas K., Vaughan K., Waterston R.,			
RA	Watson A., Weinstock L., Wilkison M., Wohldman P.,			
RA	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans."			
RL	Nature 368:32-32(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BRISTOL N2;			
RA	Clarke K., Wohldman P., Harrison M.; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.			
RA	EMBL: AF030044; AAC07951.1; -.			
DR	INTERPRO: IPR000168; -.			
DR	INTERPRO: IPR003002; -.			
DR	PFAM: PF01461; 7tm_1; 1.			
DR	SEQUENCE: 356 AA; 41323 MW; DEF906750193F6A4 CRC64;			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=BRISTOL N2;			
RA	Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.			
RA	EMBL: U40953; AAB52646.1; -.			
RA	SEQUENCE FROM N.A.			
RP	STRAIN=BRISTOL N2;			
RA	Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.			
RA	EMBL: U40953; AAB52646.1; -.			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=BRISTOL N2;			
RA	Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.			
RA	EMBL: U40953; AAB52646.1; -.			
RA	SEQUENCE FROM N.A.			
RP	STRAIN=BRISTOL N2;			
RA	Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.			
RA	EMBL: U40953; AAB52646.1; -.			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=BRISTOL N2;			
RA	Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.			
RA	EMBL: U40953; AAB52646.1; -.			
RA	SEQUENCE FROM N.A.			
RP	STRAIN=BRISTOL N2;			
RA	Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.			
RA	EMBL: U40953; AAB52646.1; -.			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=OT3;			
RA	RE			
RA	Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hino Y., Nagai Y., Sakai M., Ogura K., Otsuka R., Nakazawa H., Hosoya M., Ohfuki Y., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kishiida N., Oguchi A., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kiuchi H.,			
RA	"Complete sequence and gene organization of the genome of a hyperthermophilic archaeabacterium, Pyrococcus horikoshii OT3.;"			
RA	DNA Res. 5:55-76(1998).			
RA	RESULT			
RA	Q9VLT3			

ID	Q9VLT3	PRELIMINARY;	PRT;	1760 AA.				
AC	Q9VLT3							
DT	01-MAY-2000	(TREMBLrel. 13, Created)						
DT	01-JUN-2000	(TREMBLrel. 13, Last sequence update)						
DE	CG7586	PROTEIN.						
GN	CG7586							
OS	Drosophila melanogaster	(Fruit fly)						
Eukaryota; Metazoa; Arthropoda; tracheata; Hexapoda; Insecta;								
OC	Ephydriidae; Drosophilidae; Drosophila.							
OC	[1]							
RN		SEQUENCE FROM N.A.						
RC	STRAIN-BERKELEY;							
RX	MEDLINE; 20196006.							
RA	Amanatides M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Helderison S.N., Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandt R.C., Rogers Y.-H.C., Blazquez R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Holt G., Nelson C.R., Miklos G.L.G., Abriel H.J., Aguirre A.A., An H.-J., Andrews P.-M., Pannikar C., Baldwin D., Baldwin R.M., Basu A., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borukhov D., Botchan M.R., Bouck J., Brodtier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahake C., Davenport L.B., Davies P., De Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downs M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Fosler C., Gabriel A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibebewam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Krawitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitzky A., Li J., Li Y., Liang Y., Liu X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Miliashina N.V., Mobarry C., Morris J., Moskrefi A., Mount S.M., Moy M., Murphy L., Muzyk D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paciob J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Sildén-Klåmos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svärd R., Tector C., Turner E., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Yeh J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., zhu S., zhu X., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;							
RX	Science 287: 2185-2195 (2000).							
EMBL; AE003619; AAF52601; -.								
BASE; FBgn0031984; CG7586.								
INTERPRO; IPR000504; -.								
INTERPRO; IPR01599; -.								
INTERPRO; IPR02172; -.								
INTERPRO; IPR002890; -.								
PFAM; PF00057; LDL_recept_a; 1.								
PFAM; PF00207; A2M; 1.								
PFAM; PF01835; A2M_N; 2.								
PROSITE; PS00030; RNP_1; UNKNOWN_1.								
PROSITE; PS50088; LDLRA_2; 1.								
SEQUENCE 1760 AA; 202782 MW; B8E0602350EB7F86 CRC64;								
Db	211. VFGGLAFL 218							
RESULT	6							
ID	Q63595	PRELIMINARY;	PRT;	157 AA.				
RP	SEQUENCE FROM N.A.							
RC	TISSUE=TESTIS;							
RX	MEDLINE; 97224452.							
RA	Vanderhaegen P., Schurmans S., Vassart G., Parmentier M.; "specific repertoire of olfactory receptor genes in the male germ cells of several mammalian species"; Genomics 39:239-246 (1997).							
RT	EMBL; X89704; CAA61851.1; -.							
DR	INTERPRO; IPR000276; -.							
DR	PFAM; PF00001; 7tm_1; 1.							
FT	NON_TER 1 1.							
FT	NON_TER 157 AA; 17653 MW;							
SQ	SEQUENCE 157 AA; 17653 MW;							
Query Match	76.4%; Score 32; DB 5; Length 1760;							
Best Local Similarity	75.0%; Pred. No. 3.6e-02;							
Matches	6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;							
Qy	2 IFGSLAFL 9							
Query Match	74.4%; Score 32; DB 11; Length 221;							
Best Local Similarity	85.7%; Pred. No. 70;							
SQ	SEQUENCE 221 AA; 24719 MW;							

Matches	6;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	3 FGSLAFL 9	PRELIMINARY;	PRT;	223 AA.					
Db	189 FGSLAFM 195								
RESULT	8								
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AC	Q92IV5; 1								
DT	01-MAY-1999 (TREMBLel. 10, Created)								
DT	01-MAY-1999 (TREMBLel. 10, Last sequence update)								
DT	01-JUN-2000 (TREMBLel. 14, Last annotation update)								
ID	OLFACTORY RECEPTOR B3 (FRAGMENT).								
OS	Mus musculus (Mouse).								
OC	Eukaryota; Mela2oza; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
RN	1.1								
SEQUENCE FROM N.A.									
RP	STRAIN-BL/6; TISSUE-OLFACTORY EPITHELIUM;								
RX	MEDLINE; 9091050.								
RA	Kraulwurst D.; Yau K.W.; Reed R.R.;								
RT	"Identification of ligands for olfactory receptors by functional expression of a receptor library.";								
RL	Cell 95:917-926 (1998).								
EMBL; AF102516; AD13310.1; -.									
DR	INTERPRO; IPR000276; -.								
DR	INTERPRO; IPR000725; -.								
DR	PFAM; PF00001; 7tm.1; 1.								
DR	PRINTS; PR00237; GPRRHODOPSIN.								
DR	PRINTS; PR00245; OLFACTORYR.								
DR	PROSITE; PS00237; G-PROTEIN_RECEPTOR; UNKNOWN_1.								
KW	Receptor.								
FT	NON-TER	1	1						
FT	NON-TER	223	223						
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Best Local Similarity	85.7%;	Pred. No. 70;							
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SEQUENCE FROM N.A.									
RP	SEQUENCE FROM N.A.								
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RA	Wilson R.; Ainscough R.; Anderson K.; Baynes C.; Berks M.; Copsey T.; Cooper J.; Coulson A.; Bonfield J.; Burton J.; Connell M.; Copsey T.; Cooper J.; Coulson A.; Craxton M.; Dear S.; Du Z.; Durbin R.; Favell A.; Fulton L.; Gardner A.; Green P.; Hawkins T.; Hillier L.; Jier M.; Johnston L.; Jones M.; Kershaw J.; Kirsten J.; Lalister N.; Latrellie P.; Lightning J.; Lloyd C.; McMurray A.; Mortimore B.; O'Callaghan M.; Ralston J.; Smith A.; Sonnhammer E.; Staden R.; Sulston J.; Thierry Mieg J.; Thomas K.; Vaudin M.; Vaughan K.; Waterston R.; Watson A.; Weinstock L.; Wilkinson-Sprout J.; Wohldman P.; RT								
RT	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";								
RL	Nature 368:32-38 (1994).								
EMBL; AF07666; CAB11549.1; -.									
DR	INTERPRO; IPR001617; -.								
DR	Pfam; PF00005; ABC_tran: 1.								
SEQUENCE	454 AA;	50540 MW;	222C49339347A70C CRC64;						
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SEQUENCE FROM N.A.									
RP	SEQUENCE FROM N.A.								
RX	MEDLINE; 94150718.								
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RT	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";								
RL	Nature 368:32-38 (1994).								
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DR	INTERPRO; IPR001617; -.								
DR	Pfam; PF00005; ABC_tran: 1.								
SEQUENCE	454 AA;	50540 MW;	222C49339347A70C CRC64;						
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Best Local Similarity	66.7%;	Pred. No. 1.4e+02;							
Matches	6;	Conservative	1;	Mismatches	1;	Indels	0;	Gaps	0;
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SEQUENCE FROM N.A.									
RP	SEQUENCE FROM N.A.								
RX	MEDLINE; 94150718.								
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RT	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";								
RL	Nature 368:32-38 (1994).								
EMBL; AF07666; CAB11549.1; -.									
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RP	SEQUENCE FROM N.A.								
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RT	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";								
RL	Nature 368:32-38 (1994).								
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RL	Nature 368:32-38 (1994).								
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RT	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";								
RL	Nature 368:32-38 (1994).								
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SEQUENCE FROM N.A.									
RP	SEQUENCE FROM N.A.								
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RL	Nature 368:32-38 (1994).								
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SEQUENCE FROM N.A.									
RP	SEQUENCE FROM N.A.								
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RT	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";								
RL	Nature 368:32-38 (1994).								
EMBL; AF07666; CAB11549.1; -.									
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SEQUENCE	454 AA;	50540 MW;	222C49339347A70C CRC64;						
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Matches	6;	Conservative	1;	Mismatches	1;	Indels	0;	Gaps	0;
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SEQUENCE FROM N.A.									
RP	SEQUENCE FROM N.A.								
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RT	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";								
RL	Nature 368:32-38 (1994).					</			

Search completed: November 14, 2000, 11:55:43
 Job time: 61 sec

ILD 026659; PRELIMINARY; PRT; 232 AA.
 AC 026659; 05; Created)
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 DDT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DDT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 CONSERVED PROTEIN.
 MTH1559.
 GN Methanobacterium thermoautotrophicum.
 OS Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
 OC Methanobacterium.
 RN [1]
 RP SEQUENCE FROM N. A.
 SPANISH-DELTA_H.
 RC
 RX MEDLINE; 9807514.
 RA Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., DuBois J.,
 Aldridge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Quin D.,
 Spadafora R., Vicere R., Wang Y., Wierzbowski J., Gibson R.,
 J.Iwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 McDougal S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
 Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;
 "Complete genome sequence of Methanobacterium thermoautotrophicum
 deltaH: functional analysis and comparative genomics.";
 J. Bacteriol. 179:7135-7155 (1997).
 RL
 EMBL; AB000838; AAH85055.; -.
 DR INTERPRO; IPR002829; -.
 PFM; PF01976; DUF116; 1.
 DR
 SEQUENCE 232 AA. BREF39317F95A58ED CRC64.
 SO

RESULT	15	Q9J980	PRELIMINARY;	PRT;	264 AA.
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		Q9J980; DDT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)		
		Q9J980; DDT	YBBP FAMILY HYPOTHETICAL PROTEIN.		
		Q9J980; DDT	YBBP.		
		Q9J980; DDT	Chlamydia pneumoniae (Chlamydophila pneumoniae).		
		Q9J980; DDT	Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.		

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Scoring table:	BLOSUM62	RESULT 1
	Gapop 10.0 , Gapext 0.5	DURB_STRGW
Searched:	87993 seqs, 31947931 residues	STANDARD;
Total number of hits satisfying chosen parameters:	1088	PRT; 19 AA.
Minimum DB seq length: 0		AC P36502;
Maximum DB seq length: 20		DT 01-JUN-1994 (Rel. 29, Created)
Post-processing: Minimum Match 0%		DT 01-JUN-1994 (Rel. 29, Last sequence update)
		DT 01-FEB-1996 (Rel. 33, Last annotation update)
Post-processing: Maximum Match 100%		DE LANTIBIOTIC DURAMYCIN B.
		OS Streptoverticillium sp. (strain R2075)
Database :	Swissprot_39.*	OC Bacteria; Firmicutes; Actinobacteria; Actinomycetidae;
		OC Actinomycetales; Streptomyceae; Streptomyctaceae;
		OC Streptoverticillium.
		RN [1]
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		RX
		MDLINE: 91107436.
		RA
		Frederhagen A., Fendrich G., Markl W., Gruner J.,
		RA
		Raschidoff F., Peter H.H.,
		RA "Duramycin B and C, two new lanthionine containing antibiotics as
		RT inhibitors of phospholipase A2. Structural revision of duramycin and
		RT cinnamycin.",
		RL J. Antibiot. 43:1403-1412(1990).
		RN [2]
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		RA Zimmermann N., Freund S., Frederhagen A., Jung G.; Jung G.;
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		RA "Solution structure of the lantibiotics duramycin B and C.",
		RA "Solution structure of the lantibiotics duramycin B and C.",
		RL Eur. J. Biochem. 216:419-428(1993)
		RL (In) Schneider C.H., Eberle A.N. (eds.);
		RL Peptides 1992, pp.519-520, Eicom Science Publishers, Leiden (1993).
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		RA "Solution structure of the lantibiotics duramycin B and C.",
		RL Eur. J. Biochem. 216:419-428(1993)
		CC -1- FUNCTION: ACTS AS INHIBITOR OF PHOSPHOLIPASE A2.
		CC -1- PTM: MATURATION OF LANTIBIOTICS INVOLVES THE ENZYMIC CONVERSION OF
		CC THR, SER, AND CYS INTO DEHYDRATED AA AND THE MEMBRANE TRANSLOCATION AND
		CC BRIDGES. THIS IS FOLLOWED BY THE CLEAVAGE OF THE MODIFIED PRECURSOR.
		CC -1- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.
		KW Antibiotic; Lantibiotic.
		FT MOD_RES 4 4
		D-ALANINE.
		FT MOD_RES 6 6
		D-ALANINE (BONDED TO 19).
		FT MOD_RES 11 11
		D-ABU (AMINO BUTRIC ACID).
		FT MOD_RES 18 18
		D-ABU (AMINO BUTRIC ACID).
		FT MOD_RES 19 19
		LYSYLALANINE (BONDED TO 6).
		FT THIOETH 1 18
		ABU-S-CYS (METHYLLANTHIONINE).
		FT THIOETH 4 4
		ABU-S-CYS (METHYLLANTHIONINE).
		FT THIOETH 5 11
		ABU-S-CYS (METHYLLANTHIONINE).
		SQ SEQUENCE 19 AA; 2063 MW;
		013345E27362F00 CRC64;
		Query Match 51.2%; Score 22; DB 1; Length 19;
		Best Local Similarity 57.1%; Pred. No. 1.6e+02;
		Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
		Qy 3 FGSLAFL 9

Db 7 | | |: 7 EGPLTFV 13

RESULT 2 UN06_PINPS STANDARD; PRT; 7 AA.

TD UN06_PINPS STANDARD; PRT; 7 AA.

AC P81075; ID UP51_UPEIN STANDARD; PRT; 13 AA.

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE UNKNOWN PROTEIN FROM 2D-PAGE OF NEEDLES (NI41) (FRAGMENT).

OS Pinus pinaster (Maritime Pine).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.

[1]

RN PRT; 13 AA.

RP SEQUENCE.

RC TISSUE=NEEDLE;

RX MEDLINE: 9927408B.

RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrmann N., Kremer A., Frigerio J.-M., Plomion C.; "Separation and characterization of needle and xylem maritime pine proteins.", Electrophoresis 20:1098-1108(1999).

RL Electrophoresis 20:1098-1108(1999).

CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 6.6, ITS MW IS: 25 kDa.

FT NON-TER 1 1

FT NON-TER 7 7

SQ SEQUENCE 7 AA; 823 MW; 69D767244865740 CRC64;

Query Match 48.8%; Score 21; DB 1; Length 7;

Best Local Similarity 42.9%; Pred. No. 8.8e+04;

Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0; Gaps 0;

Qy 2 IFGSLAF 8

Db 1 LYGNLJPF 7

RESULT 3 CRBL_VESTR STANDARD; PRT; 13 AA.

AC P17231; ID UP51_UPEIN STANDARD; PRT; 13 AA.

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE VESPID CHEMOTACTIC PEPTIDE T (VESPCT-1).

OS Vespa tropica (Hornet).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea; Vespidae; Vespinae; Vespae.

[1]

RP SEQUENCE.

RC TISSUE=VENOM;

RA Yasuha T., Nakajima T., Ersperer V.; (In) Sakakibara S. (eds.); Peptide Chemistry 1982, pp.213-218, Protein Research Foundation, Osaka (1983).

CC -!- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS OF NEUTROPHILS.

KW Mast cell degranulation; Chemotaxis; Venom; Amidation.

FT MOD_RES 13 13

SEQUENCE 13 AA; 1354 MW; 220140365DFE338 CRC64;

Query Match 44.2%; Score 19; DB 1; Length 13;

Best Local Similarity 66.7%; Pred. No. 4.7e+02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Gaps 0;

Qy 1 KIFGSL 6

Db 7 KIUGGL 12

RESULT 4 UP51_UPEIN STANDARD; PRT; 13 AA.

AC P8036; ID UP51_UPEIN STANDARD; PRT; 13 AA.

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE UPBRIN 5.1.

OS Uperoleia inundata (Floodplain toadlet).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae; Uperoleia.

[1]

RN PRT; 13 AA.

RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=SKIN SECRETION;

RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C., Adams G.W., Severini C.; "Novel uperolein peptides from the dorsal glands of the australian floodplain toadlet Uperoleia inundata.";

RT Aust. J. Chem. 49:475-484(1996).

RL -!- FUNCTION: UNKNOWN.

CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.

CC -!- MASS SPECTROMETRY: MW=1426; METHOD=FAST

KW Amphibian skin.

SEQUENCE 13 AA; 1457 MW; 290CA148C384B5A7 CRC64;

Query Match 44.2%; Score 19; DB 1; Length 13;

Best Local Similarity 75.0%; Pred. No. 4.7e+02;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Gaps 0;

Qy 2 IFGFS 5

Db 1.0 VFGS 13

RESULT 5 GR75_CANFA STANDARD; PRT; 14 AA.

AC P9502-CANFA

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE MITOCHONDRIAL STRESS-70 PROTEIN (75 kDa GLUCOSE REGULATED PROTEIN) (GRP 75) (FRAGMENT).

GN HSP9.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; carnivora; Fissipedia; Canidae; Canis.

[1]

RP SEQUENCE.

RC TISSUE=HEART;

RX MEDLINE: 98163340.

RA Dunn M.J., Corbett J.M., Wheeler C.H.; "HSC-2DPAGE and the two-dimensional gel electrophoresis database of dog heart proteins.";

RT RT Electrophoresis 18:2795-2802(1997).

CC -!- FUNCTION: IMPLICATED IN THE CONTROL OF CELL PROLIFERATION AND CELLULAR AGING. MAY ALSO ACT AS A CHAPERONE.

CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL.

CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

CC HSC-2DPAGE; P99502; DOG.

DR DR INTERPRO; IPF001023;

DR PROSITE; PS00297; HSP70_1; PARTIAL.

DR PROSITE; PS00329; HSP70_2; PARTIAL.

DR PROSITE; PS01036; HSP70_3; PARTIAL.

KW ATP-binding; Mitochondrion.

FT NON-TER 14 14

SEQUENCE 14 AA; 1438 MW; 2AAEDDIAACBAC8D8 CRC64;

Query Match 44.2%; Score 19; DB 1; Length 14;
 Best Local Similarity 37.5%; Pred. No. 5.1e+02; Gaps 0;
 Matches 3; Conservative 2; Indels 0; Gaps 0;
 RT
 Qy 2 IFGSLAFL 9
 DR 111:::
 DB 5 IFGAVVXI 12

RESULT 6

PHPT_PSEPE PHPT_PSEPE STANDARD; PRT; 18 AA.
 ID PHPT_PSEPE STANDARD; PRT; 18 AA.
 AC 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-MAY-1992 (Rel. 22, Last annotation update)
 DE PHERMONOTROPIN (PSS-PT)
 OS Pseudocletta separata (Armyworm).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 Noctuoidea; Noctuidae; Hadeninae; Pseudaletia.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=HEAD;
 RX MEDLINE; 92134266.
 RA Matsumoto S., Fonagy A., Kurihara M., Uchiumi K., Nagamine T.,
 RA Chijimatsu M., Mitsu T.,
 RR "isolation and primary structure of a novel pheromonotropic
 neuropeptide structurally related to leucopyrokinin from the armyworm
 larvae, *Pseudaletia separata*."
 RT Biophys. Res. Commun. 182:534-539 (1992).
 CC -1- FUNCTION: HORMONE THAT CONTROLS SEX PHEROMONE PRODUCTION IN
 LARVAE.
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR PIR: JS0647; JS0647.
 DR INTERPRO: IPR01484; -
 DR PS00539; PYROKININ; 1.
 KW Hormone; Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 18 18 AMIDATION.
 SQ SEQUENCE 18 AA; 2200 MW; DDF3A1B75ACB18FF CRC64;

Query Match 44.2%; Score 19; DB 1; Length 18;
 Best Local Similarity 37.5%; Pred. No. 6.5e+02; Gaps 0;
 Matches 3; Conservative 2; Indels 0; Gaps 0;
 RT
 Qy 1 KIFGSLAFL 8
 DR 1:::
 DB 7 KVENVF 14

RESULT 7

DURA_STRGV DURA_STRGV STANDARD; PRT; 19 AA.
 ID DURA_STRGV STANDARD; PRT; 19 AA.
 AC P36504;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DE LANTIBIOTIC DURAMYCIN (LEUCOPEPTRIN) (ANTIBIOTIC PA48009).
 OS Streptoverticillium griseoverticillatum.
 OC Bacteria; Firmicutes; Actinobacteria; Actinomycetidae;
 Actinomycetales; Streptomyces; Streptomyctaceae;
 Streptoverticillium.
 RN SEQUENCE, AND STRUCTURE BY NMR.
 RC STRAIN=PA-48009;
 RX MEDLINE; 91107438.
 RA Hayashi F., Nagashima K., Terui Y., Kawamura Y., Matsumoto K.,
 Itazaki H.;
 RL "the structure of PA48009: the revised structure of duramycin."
 RN [2]
 RN SEQUENCE.

RX MEDLINE; 91107436.
 RA Friedenhausen A., Fendrich G., Marki F., Marki W., Gruner J.,
 Raschdorff F., Peter H.H.;
 RT "Duramycins B and C, two new lanthionine containing antibiotics as
 inhibitors of phospholipase A2. Structural revision of duramycin and
 cinnamycin.";
 RL J. Antibiot. 43:1403-1412 (1990).
 CC -1- FUNCTION: ACTS AS INHIBITOR OF PHOSPHOLIPASE A2.
 CC -1- PTM: MATURATION OF LANTIBIOTICS INVOLVES THE ENZYMIC CONVERSION OF
 SULFIDE
 CC BRIDGES, THIS IS FOLLOWED BY THE FORMATION OF SULFIDE
 CC CLEAVAGE OF THE MODIFIED PRECURSOR.
 CC -1- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.
 KW Antibiotic; Lantibiotic.
 FT MOD_RES 4 4 D-ALANINE.
 FT MOD_RES 6 6 D-ALANINE (BONDED TO 19).
 FT MOD_RES 11 11 D-ABU (AMINOBUTYRIC ACID).
 FT MOD_RES 18 18 D-ABU (AMINOBUTYRIC ACID).
 FT MOD_RES 19 19 LYSINGALANINE (BONDED TO 6).
 FT THIOTH 1 18 ABU-S-CYS (METHYLLANTHIONINE).
 FT THIOTH 4 14 ALA-S-CYS (LANTHIONINE).
 FT THIOTH 5 11 ABU-S-CYS (METHYLLANTHIONINE).
 SQ SEQUENCE 19 AA; 2069 MW; 012951AE27362F00 CRC64;

Query Match 41.9%; Score 18; DB 1; Length 19;
 Best Local Similarity 42.9%; Pred. No. 1.1e+03;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 FGSLAFL 9
 DR 7 FGPFVFV 13

RESULT 8

NUDM_CANFA NUDM_CANFA STANDARD; PRT; 12 AA.
 ID P54713;
 AC 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE NADH-UBIQUINONE OXIDOREDUCTASE 42 KDA SUBUNIT (EC 1.6.5.3)
 DE (EC 1.6.99.3) (COMPLEX I-42KD) (FRAGMENT).
 GN NDUFAL0
 OS Canis familiaris (Dog).
 OC Euksaryota; Metzoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=HEART;
 RX MEDLINE; 98163340.
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 dog heart proteins.";
 RT Electrophoresis 18:2795-2802 (1997).
 CC -1- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
 CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
 TO BE UBIQUINONE.
 CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+). + UBIQUINOL.
 CC -1- COFACTOR: FAD; CONTAINS ONE NONCOVALENTLY BOUND FAD PER
 POLYPEPTIDE CHAIN.
 CC -1- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS.
 CC THIS A COMPONENT OF THE HYDROPHOBIC PROTEIN FRACTION.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
 DR HSC-2DPAGE; P54713; DOG.
 KW Oxidoreductase; NAD; Ubiquinone; Flavoprotein; FAD; Mitochondrion.
 FT NON-TER 12 12
 SQ SEQUENCE 12 AA; 1284 MW; 3CCD4E2B36EDD737 CRC64;

Query Match 39.5%; Score 17; DB 1; Length 12;
 Best Local Similarity 42.9%; Pred. No. 1.1e+03;
 Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 FGSLAFL 9
Db 3 YGPIAXI 9

RESULT 9
CRBL_VESAN STANDARD; PRT; 13 AA.
ID CRBL_VESAN
AC P17233;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE VESPID CHEMOTACTIC PEPTIDE A (VESCP-A).
OS Vespa analis (Hornet).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
Vespidae; Vespinae; Vespiidae; Vespiinae; Vespa.
[1]
RN PSEQUENCE;
RC TISSUE=VENOM;
RA Yasuura T., Nakajima T., Fukuda K., Tsukamoto Y., Mori M., Kitada C.,
RA Fujino M.;
RL (In) Munekata E. (eds.);
RL Peptide Chemistry 1983, pp.185-190, Protein Research Foundation,
Osaka (1984).
CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS
OF NEUTROPHILS.
KW Mast cell degranulation; Chemotaxis; Venom; Amidation.
FT MOD_RES 13 13 MW: C85554365DF9233D CRC64;
SEQUENCE 13 AA; 1386 MW;

Query Match 39.5%; Score 17; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KIFGSL 6
Db 7 KLGGL 12

RESULT 10
CRBL_VESXA STANDARD; PRT; 13 AA.
ID CRBL_VESXA
AC P17234;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE VESPID CHEMOTACTIC PEPTIDE X (VESCP-X).
OS Vespa xanthoptera (Japanese hornet).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
Vespidae; Vespinae; Vespiidae; Vespiinae; Vespa.
[1]
RN PSEQUENCE;
RC TISSUE=VENOM;
RA Yasuura T., Itokawa H., Suzuki N., Nakamura H., Nakajima T.,
RL (In) Izumiya N. (eds.);
RL Peptide Chemistry 1984, pp.177-182, Protein Research Foundation,
Osaka (1985).
CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS
OF NEUTROPHILS.
KW Mast cell degranulation; Chemotaxis; Venom; Amidation.
FT MOD_RES 13 13 MW: C85040365DF9233D CRC64;
SEQUENCE 13 AA; 1368 MW;

Query Match 39.5%; Score 17; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KIFGSL 6

Db 1: 1 1
Db 7 KLGGL 12

RESULT 11
LMA2_LOCMI STANDARD; PRT; 15 AA.
ID LMA2_LOCMI
AC P30497;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE L0H-AG-MYOTROPIN II (ACCESSORY GLAND MYOTROPIN II).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC Acridomorpha; Acridoidea; Acrididae; Locusta.
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=MALE ACCESSORY GLAND;
RA Pamien L., Schools L., Proost P., Decock B., de Loof A.;
RT Isolation, identification and synthesis of L0H-AG-myotropin [L.^a
RT novel peptide in the male accessory reproductive glands of Locusta
migratoria.];
RT Insect Biochem. 21:243-248(1991).
RL Insect Biochem. 21:243-248(1991).
CC -1- FUNCTION: MYOTROPIC PEPTIDE.
CC -1- TISSUE SPECIFICITY: MALE ACCESSORY GLANDS.
KW Neuropeptide.
SQ SEQUENCE 15 AA; 1592 MW; BC800FF4B41941CF CRC64;

Query Match 39.5%; Score 17; DB 1; Length 15;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 FGSL 6
Db 9 FGNL 12

RESULT 12
UPAR_HUMAN STANDARD; PRT; 16 AA.
ID UPAR_HUMAN
AC P31935;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF PLASMA (S907 53) (FRAGMENTS).
OS Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE.
RC TISSUE=PLASMA;
RX MEDLINE: 94147970.
RA Golaz O., Hughes G.J., Frutiger S., Paquet N., Balroch A.,
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Appel R.D., Walzer C.,
RA Ballant L., Hochstrasser D.F.;
RT "Plasma and red blood cell protein maps: update 1993. ";
RL Electrophoresis 14:1223-1231(1993).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 4.9. ITS MW IS: 41 KDA.
DR SWISS-2DPAGE: P31935; HUMAN.
FT NON_TER 1
FT NON_CONS 7 8
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1879 MW; D63C5047818114B2 CRC64;

Query Match 39.5%; Score 17; DB 1; Length 16;
Best Local Similarity 57.1%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 FGSLAFL 9

Db	4	FLXAYL 10	RESULT 13	PSP3_PHYPA	STANDARD;	PRT;	12 AA.	Query Match	37.2%; Score 16; DB 1; Length 13;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.
AC	P80662;		AC	PSP3_PHYPA	STANDARD;	PRT;	12 AA.	Best Local Similarity 50.0%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II; Chloroplast; Thylakoid membrane.	
DR	01-OCT-1996 (Rel. 34, Created)		DR	PSP3_PINYPS	STANDARD;	PRT;	13 AA.	Query Match	37.2%; Score 16; DB 1; Length 13;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.
DT	01-OCT-1996 (Rel. 34, Last sequence update)		DT	PSP3_PINYPS	STANDARD;	PRT;	13 AA.	Best Local Similarity 50.0%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II; Chloroplast; Thylakoid membrane.	
DT	01-NOV-1997 (Rel. 5, Last annotation update)		DT	PSP3_PINYPS	STANDARD;	PRT;	13 AA.	Query Match	37.2%; Score 16; DB 1; Length 13;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.
DE	OXYGEN-EVOLVING ENHANCER PROTEIN 2 (OEE2) (24 KDA SUBUNIT OF OXYGEN		DE	PSP3_PINYPS	STANDARD;	PRT;	13 AA.	Best Local Similarity 50.0%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).	
DE	EVOLVING SYSTEM OF PHOTOSYSTEM II (FRAGMENT).		DE	PSP3_PINYPS	STANDARD;	PRT;	13 AA.	Query Match	37.2%; Score 16; DB 1; Length 13;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.
OS	physcomitrella patens (Moss).		OS	PSP3_PINYPS	STANDARD;	PRT;	13 AA.	Best Local Similarity 50.0%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).	
OC	Eukaryota; Viridiplantae; Embryophyta; Bryophyta; Bryopsida;		OC	PSP3_PINYPS	STANDARD;	PRT;	13 AA.	Query Match	37.2%; Score 16; DB 1; Length 13;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.
OC	Funariidae; Funariales; Funariaceae; Physcomitrella.		OC	PSP3_PINYPS	STANDARD;	PRT;	13 AA.	Best Local Similarity 50.0%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).	
RN	[1]		RN	[1]		RESULT 15		Query Match	37.2%; Score 16; DB 1; Length 13;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.
RP			RP	UC18_MAIZE	STANDARD;	PRT;	14 AA.	Best Local Similarity 50.0%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).	
RC	SEQUENCE: PROTONEMEA.		RC	UC18_MAIZE	STANDARD;	PRT;	14 AA.	Query Match	37.2%; Score 16; DB 1; Length 13;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.
RD	9/27/5459.		RD	P80624;				Best Local Similarity 50.0%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).	
RA	Kasten B., Buck F., Nuske J., Reski R.;		RA	P80624;				Query Match	37.2%; Score 16; DB 1; Length 13;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.
RT	"Cytokinin affects nuclear- and plastome-encoded energy-converting		RT	01-OCT-1996 (Rel. 34, Created)				Best Local Similarity 50.0%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).	
RT	plastid enzymes".		RT	01-OCT-1996 (Rel. 34, Last sequence update)				Query Match	37.2%; Score 16; DB 1; Length 13;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.
RL	Planta 201:261-272(1997).		RL	01-OCT-1996 (Rel. 34, Last annotation update)				Best Local Similarity 50.0%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).	
CC	-1 - FUNCTION: ASSOCIATED WITH THE OXYGEN-EVOLVING COMPLEX OF		CC	UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLATED COLEOPTILE (SPOT 263)				Query Match	37.2%; Score 16; DB 1; Length 13;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.
CC	CHLOROPLAST THYLAKOID MEMBRANE; ASSOCIATED		CC	DE (FRAGMENT).				Best Local Similarity 50.0%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).	
CC	WITH THE PHOTOSYSTEM II COMPLEX.		CC	DE (FRAGMENT).				Query Match	37.2%; Score 16; DB 1; Length 13;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.
CC	-1 - INDUCTION: BY LIGHT.		CC	DE (FRAGMENT).				Best Local Similarity 50.0%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).	
CC	-1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.		CC	DE (FRAGMENT).				Query Match	37.2%; Score 16; DB 1; Length 13;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.
CC	Photosynthesis; Photosystem II; Chloroplast; Thylakoid membrane;		CC	DE (FRAGMENT).				Best Local Similarity 50.0%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).	
KW	Multigene family.		CC	DE (FRAGMENT).				Query Match	37.2%; Score 16; DB 1; Length 13;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.
KW			CC	DE (FRAGMENT).				Best Local Similarity 50.0%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).	
NON_TER	12		NON_TER	12		Query Match	37.2%; Score 16; DB 1; Length 12;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.		
SEQUENCE	12 AA;		SEQUENCE	1182 MW;	8D2B0D54D7C44DC5 CRC64;	Best Local Similarity 50.0%; Pred. No. 1.3e+03; Mismatches 2; Indels 0; Gaps 0;	Best Local Similarity 50.0%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).		
Qy	2 IFGS 5		Qy	2 IFGS 5		Query Match	37.2%; Score 16; DB 1; Length 12;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.		
Db	:1: 11: 8 VGA 11		Db	:1: 11: 8 VGA 11		Best Local Similarity 50.0%; Pred. No. 1.3e+03; Mismatches 2; Indels 0; Gaps 0;	Best Local Similarity 50.0%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).		
RESULT 14	PSBP_PINYPS	STANDARD;	RESULT 14	PSBP_PINYPS	STANDARD;	PRT;	13 AA.	Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.
ID	PSBP_PINYPS	STANDARD;	ID	PSBP_PINYPS	STANDARD;	PRT;	13 AA.	Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).	
AC	P81668;		AC	P81668;		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.		
DT	15-JUL-1999 (Rel. 38, Created)		DT	15-JUL-1999 (Rel. 38, Last sequence update)		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
DT	15-JUL-1999 (Rel. 38, Last annotation update)		DT	15-JUL-1999 (Rel. 38, Last annotation update)		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.		
DE	OXYGEN-EVOLVING ENHANCER PROTEIN 2 (OEE2) (23 KDA SUBUNIT OF OXYGEN		DE	OXYGEN-EVOLVING ENHANCER PROTEIN 2 (OEE2) (23 KDA SUBUNIT OF OXYGEN		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
DE	EVOLVING SYSTEM OF PHOTOSYSTEM II (FRAGMENT).		DE	EVOLVING SYSTEM OF PHOTOSYSTEM II (FRAGMENT).		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.		
GN	PSBP.		GN	PSBP.		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.		
OS	Pinus pinaster (Maritime Pine).		OS	Pinus pinaster (Maritime Pine).		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermato phyta;		OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermato phyta;		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.		
OC	Coniferopsida; Coniferales; pinaceae; pinus.		OC	Coniferopsida; Coniferales; pinaceae; pinus.		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
RN	[1]		RN	[1]		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.		
RP			RP			Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
RC	TISSUE-NEEDLE;		RC	TISSUE-NEEDLE;		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.		
RX	MEDLINE: 99274088.		RX	MEDLINE: 99274088.		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
RA	Costa P., Piloni C., Bauw G., Dubos C., Bahman N., Kremer A.,		RA	Costa P., Piloni C., Bauw G., Dubos C., Bahman N., Kremer A.,		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - FUNCTION: ASSOCIATED WITH THE OXYGEN-EVOLVING COMPLEX OF		
RA	Frigerio J.-M., Piloni C.; Pinaceae; pinus.		RA	Frigerio J.-M., Piloni C.; Pinaceae; pinus.		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
RA	Separation and characterization of needle and xylem maritime pine		RA	Separation and characterization of needle and xylem maritime pine		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.		
RT	proteins".		RT	proteins".		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
RT	Electrophoresis 20:1098-1108(1999).		RT	Electrophoresis 20:1098-1108(1999).		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - FUNCTION: ASSOCIATED WITH THE OXYGEN-EVOLVING COMPLEX OF		
CC	PHOTOSYSTEM II (BY SIMILARITY).		CC	PHOTOSYSTEM II (BY SIMILARITY).		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
CC	SURCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE; ASSOCIATED		CC	SURCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE; ASSOCIATED		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.		
CC	WITH THE PHOTOSYSTEM II COMPLEX (BY SIMILARITY).		CC	WITH THE PHOTOSYSTEM II COMPLEX (BY SIMILARITY).		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
CC	-1 - MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN		CC	-1 - MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN		
CC	(SPOT N179) IS: 5.9. ITIS MW IS: 22 KDA.		CC	(SPOT N179) IS: 5.9. ITIS MW IS: 22 KDA.		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
CC	DE (PYRPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) (FRAGMENT).		CC	DE (PYRPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) (FRAGMENT).		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN		
CC	DE (PPAC).		CC	DE (PPAC).		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
CC	PPAC-BACME	STANDARD;	CC	PPAC-BACME	STANDARD;	PRT;	16 AA.	Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.
ID	P56948;		ID	P56948;		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
AC			AC			Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.		
DT	30-MAY-2000 (Rel. 39, Created)		DT	30-MAY-2000 (Rel. 39, Last sequence update)		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
DT	30-MAY-2000 (Rel. 39, Last annotation update)		DT	30-MAY-2000 (Rel. 39, Last annotation update)		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.		
DE	MANGANESE-DEPENDENT INORGANIC PYROPHOSPHATE (EC 3.6.1.1).		DE	MANGANESE-DEPENDENT INORGANIC PYROPHOSPHATE (EC 3.6.1.1).		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
GN	PPAC.		GN	PPAC.		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.		
OS	Bacillus megaterium.		OS	Bacillus megaterium.		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
OC	Bacteri: Firmicutes; Bacillus/Clostridium group;		OC	Bacteri: Firmicutes; Bacillus/Clostridium group;		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.		
OC	Bacillus/Spa thylococcus group; Bacillus.		OC	Bacillus/Spa thylococcus group; Bacillus.		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
RN	[1]		RN	[1]		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.		
RP			RP			Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
RX	SEQUENCE.		RX	SEQUENCE.		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - SIMILARITY: TO OTHER OEE2 SUBUNITS.		
RA	Young T.W., Kuhn N.J., Wadeson A., Burges D., Cooke G.D.;		RA	Young T.W., Kuhn N.J., Wadeson A., Burges D., Cooke G.D.;		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
RA	"Bacillus subtilis" OR YrbQ encodes a manganese-dependent inorganic		RA	"Bacillus subtilis" OR YrbQ encodes a manganese-dependent inorganic		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN		
RA	pyrophosphatase with dissociative properties?"		RA	pyrophosphatase with dissociative properties?"		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
RT	RT		RT	RT		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN		
RT	RT		RT	RT		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
RT	RT		RT	RT		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN		
RT	RT		RT	RT		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
RT	RT		RT	RT		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN		
RT	RT		RT	RT		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
RT	RT		RT	RT		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN		
RT	RT		RT	RT		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
RT	RT		RT	RT		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN		
RT	RT		RT	RT		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
RT	RT		RT	RT		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN		
RT	RT		RT	RT		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
RT	RT		RT	RT		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN		
RT	RT		RT	RT		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
RT	RT		RT	RT		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN		
RT	RT		RT	RT		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
RT	RT		RT	RT		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN		
RT	RT		RT	RT		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
RT	RT		RT	RT		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN		
RT	RT		RT	RT		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
RT	RT		RT	RT		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN		
RT	RT		RT	RT		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
RT	RT		RT	RT		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN		
RT	RT		RT	RT		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
RT	RT		RT	RT		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN		
RT	RT		RT	RT		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
RT	RT		RT	RT		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN		
RT	RT		RT	RT		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
RT	RT		RT	RT		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN		
RT	RT		RT	RT		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
RT	RT		RT	RT		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN		
RT	RT		RT	RT		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
RT	RT		RT	RT		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN		
RT	RT		RT	RT		Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;	KW Photosynthesis; Photosystem II (FRAGMENT).			
RT	RT		RT	RT		Query Match	37.2%; Score 16; DB 1; Length 14;	CC -1 - MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED		

RL Microbiology 144:2563-2571(1998)
 CC -1 CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -1 COFACTOR: REQUIRES MANGANESE FOR ITS ACTIVITY.
 CC -1 SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1 SIMILARITY: BELONGS TO THE PPASE CLASS C FAMILY.
 KW Hydrolase; Manganese.
 FT NON-TER 16 16 AA; 1828 MW; 3C0E6735D98B38A0 CRC64;
 SQ SEQUENCE 16 AA: ||| 16 AA;

Query Match 37.28; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 IFG 4
 Db 5 IFG 7

RESULT 17
 ATP1_PAVLU STANDARD; PRT; 17 AA.
 ID ATP1_PAVLU STANDARD; PRT; 17 AA.
 AC P28529;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE ATP SYNTHASE A CHAIN (EC 3.6.1.34) (SUBUNIT IV) (FRAGMENT).
 GN ATP1a
 OS Pavlova lutherii (Monochrysis lutheri).
 OC Chloroplast.
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92116212.
 RA Scaramuzzi C.D., Stokes H.W., Hiller R.G.;
 RT "Characterisation of a chloroplast-encoded secy homologue and atpH
 from a chromophytic alga. Evidence for a novel chloroplast genome
 organisation";
 RL FEBS Lett. 304:119-123(1992).
 CC -1 FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL; IT MAY PLAY A
 CC DIRECT ROLE IN THE TRANSLOCATION OF PROTONS ACROSS THE MEMBRANE.
 CC -1 SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
 CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
 CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
 CC HAS THREE MAIN SUBUNITS: A, B AND C.
 CC -1 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. CHLOROPLAST
 CC -1 SIMILARITY: BELONGS TO THE ATPASE A CHAIN FAMILY.
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 CC or send an email to license@isb-sib.ch).
 DR PIR: 264731; CA45996.1; -.
 DR MENDL; 2272; PAVLU; atp1; 1.
 DR INNERTPRO; IPR000568; -.
 DR PROSITE; PS00449; ATPASE_A; PARTIAL.
 KW Hydrogen ion transport; CF(0); Chloroplast; Transmembrane.
 FT NON-TER 1 13 POTENTIAL.
 FT TRANSMEM <1 13
 SQ SEQUENCE 17 AA: ||| 1753 MW; F313DCE74C23CF2E CRC64;

Query Match 37.28; Score 16; DB 1; Length 17;
 Best Local Similarity 50.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 2 IFGSLA 7

Db 11 : 1; 3 IFATLS 8

RESULT 18
 AHD2_TEPY STANDARD; PRT; 18 AA.
 ID AHD2_TEPY
 AC P34430;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE 20-ALPHA-HYDROXYSTEROID DEHYDROGENASE (EC 1.1.1.149) (20-ALPHA-HSD)
 DE (FRAGMENT).
 OS tetrahydema pyriformis.
 OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
 OC Tetrahydema; Tetrahydema.
 RN [1.]
 RP SEQUENCE AND CHARACTERIZATION.
 RC SPBAIN-N;
 RX MEDLINE: 94107273.
 RA Inazu A., Saito K., Nakayama Y., Hara A., Nozawa Y.;
 RT "Purification and characterization of a novel dimeric 20 alpha-hydroxysteroid dehydrogenase from Tetrahydema pyriformis. ";
 RL Biochem. J. 297:195-200(1994).
 CC -1 FUNCTION: SPECIFIC FOR THE OXIDATION OF THE 20-ALPHA HYDROXY
 CC GROUP OF 17-ALPHA-HYDROXYPROGESTERONE AND 17-ALPHA-HYDROXYPREGNENOLONE.
 CC -1 CATALYTIC ACTIVITY: 17-ALPHA,20-ALPHA-DIHYDROXYPROGESTERONE + NAD(P)H
 CC -1 NAD(P)(+); 17-ALPHA-HYDROXYPROGESTERONE + NAD(P)H.
 CC -1 SUBUNIT: HOMODIMER.
 DR PIR: SA0502; SA0502.
 KW Oxidoreductase; NADP.
 FT NOLTER 18
 SQ SEQUENCE 18 AA: ||| 1861 MW; 16DF6B267E3B0A0D CRC64;

Query Match 37.28; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IFG 4
 Db 15 IFG 17

RESULT 19
 NPA_BOVIN STANDARD; PRT; 18 AA.
 ID NPA_BOVIN
 AC P15506;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-APR-1990 (Rel. 14, Last annotation update)
 DE NEUROPEPTIDE A.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Gertariodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 RN [1.]
 RP SEQUENCE.
 RC T15SUB-BRAIN;
 RX MEDLINE: 86067985.
 RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
 RT Isolation, sequencing, synthesis, and pharmacological
 RT characterisation of two brain neuropeptides that modulate the action
 RT of morphine. ";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
 CC -1 FUNCTION: MODULATES THE ACTION OF MORPHINE.
 DR PIR: A24749; A24749.
 KW Neuropeptide; Amidation.
 FT SIMILAR 15 18
 FT MOD_RES 18 18
 SQ SEQUENCE 18 AA: ||| 1921 MW; EC52DAE1F45CFCFB CRC64;

Query Match 37.2%; Score 16; DB 1; Length 18;
 Best Local Similarity 80.0%; Pred. No. 2.7e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 FGSLA 7
 Db 9 FWSLA 13

RESULT 20
 SEAH_HELAN STANDARD PRT; 18 AA.
 ID SEAH_HELAN
 AC P81098;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE SEED FATTY ACYL-ESTER HYDROLASE (EC 3.1.1.1) (FRAGMENT).
 OS Helianthus annuus (Common sunflower).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicots; core eudicots; Asteridae;
 euanthids II; Asterales; Asteraceae; Asteroideae; Helianthae;
 OC Helianthus.
 RN [1]
 RP SEQUENCE.
 RC STRAIN=CV. RUSTICA / VAR. EUROFLOR; TISSUE=SEED;
 RA Belison F., Gardies A.-M., Teisseire M., Ferre N., Noat G.;
 RT "An esterase neosynthesized in post-germinated sunflower seeds is
 related to a new family of lipolytic enzymes.";
 RL Plant Physiol. 35:761-765(1977).
 RN [2]
 RP CHARACTERIZATION.
 RX CHARLINE; 95210327.
 RA Teisseire M., Borel M., Cailliol B., Mari J., Gardies A.-M., Noat G.;
 RT "Purification and characterization of a fatty acyl-ester hydrolase
 from post-germinated sunflower seeds.";
 RL Biochim. Biophys. Acta 1255:105-112 (1995).
 CC -!- FUNCTION: IMPLICATED IN THE BREAKDOWN OF OIL BODY-STORED LIPIDS
 DURING POST-GERMINATION.
 CC -!- CATALYTIC ACTIVITY: A CARBOXYLIC ESTER + H(2)O = AN ALCOHOL + A
 CC CARBOXYLIC ANION.
 CC -!- TISSUE SPECIFICITY: SEED.
 CC -!- DEVELOPMENTAL STAGE: POST-GERMINATION.
 CC -!- SIMILARITY: BELONGS TO THE "GDSL" FAMILY OF LIPOLYtic ENZYMES.
 DR INTERPRO; IPRO01087; -.
 PRoteIN; PS01098; LIPASE_GDSL_SER; PARTIAL.
 KW Hydrolase; Lipid degradation; Glycoprotein.
 ACT_SITE 13 BY SIMILARITY.
 FT NON-TER 18 18
 SEQUENCE 18 AA; 2057 MW; 3E9A80E6548E862 CRC64;

Query Match 37.2%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IFG 4
 Db 9 IFG 11

RESULT 21
 IBB2_UROHAA STANDARD PRT; 19 AA.
 ID IBB2_UROHAA
 AC P18932;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DE HEMOGLOBIN BETA-2 CHAIN (FRAGMENT).
 OS Uromastyx harwickii (Indian spiny-tailed lizard).
 OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Lepidosauria; Squamata; Iguanidae; Agamidae; Leiocephinae;
 Uromastyx.

RN [1]
 RP SEQUENCE.
 RX MEDLINE; 84029159.
 RA Nagvi S., Zaidi Z.H., von Bahr-Lindstroem H., Carlquist M.,
 RA Jernvall H.;
 RT "Characterization of hemoglobin from the lizard Uromastyx
 harwickii.";
 RL FEBS Lett. 162:290-295(1983).
 DR PIR; A05305; A05305.
 DR INTERPRO; IPRO00971; -.
 DR PROSITE; PS01033; GLOBIN; PARTIAL.
 KW Heme; Oxygen transport; Respiratory protein; Erythrocyte.
 FT NON-TER 19
 SQ SEQUENCE 19 AA; 1914 MW; C40AD8EA30019057 CRC64;

Query Match 37.2%; Score 16; DB 1; Length 19;
 Best Local Similarity 40.0%; Pred. No. 2.8e+03;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FGSLA 7
 Db 5 FGNIS 9

RESULT 22
 HHP_THICU STANDARD PRT; 19 AA.
 ID HHP_THICU
 AC P80487;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE HETEROTROPH-SPECIFIC PROTEIN (FRAGMENT).
 OS Thiobacillus cuprinus.
 OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Thiomonas.
 RN [1]
 RP SEQUENCE.
 RC STRAIN=DSM 5494;
 RA Martin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;
 RL Submitted (SEP-1995) to the SWISS-PROT data bank.
 CC -!- MISCELLANOUS: FOUND SPECIFICALLY IN CELLS CULTURED
 HETEROTROPHICALLY.
 FT NON-TER 19
 SQ SEQUENCE 19 AA; 1786 MW; C549197D0A492B07 CRC64;

Query Match 37.2%; Score 16; DB 1; Length 19;
 Best Local Similarity 50.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IFG 7
 Db 8 VIGSAA 13

RESULT 23
 LANC_STRSQ STANDARD PRT; 19 AA.
 ID LANC_STRSQ
 AC P38655;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE LANTIBIOTIC ANCOVENIN.
 OS Streptomyces sp. (strain N647P-2).
 OC Bacteria; Firmicutes; Actinobacteria; Streptomyctaceae; Streptomyces.
 RN [1]
 RP SEQUENCE.
 RA Wakamiya T., Ueki Y., Shiba T., Kido Y., Motoiki Y.;
 RT "The structure of ancovenin, a new peptide inhibitor of angiotensin I
 converting enzyme.";
 RT Tetrahedron Lett. 26:665-668(1985).
 RL

CC -1- FUNCTION: ACTS AS INHIBITOR OF ANGIOTENSIN I CONVERTING ENZYME.
 CC -1- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.
 DR PIR: AG1284 ; EWSMAN.
 KW Antibiotic; Lantibiotic.
 FT MOD_RES 4 4 D-ALANINE.
 FT MOD_RES 6 6 D-ALANINE (BONDED TO 19).
 FT MOD_RES 11 11 D-ABU (AMINOBUTYRIC ACID).
 FT MOD_RES 18 18 D-ABU (AMINOBUTYRIC ACID).
 FT MOD_RES 19 19 LYSINOALANINE (BONDED TO 6).
 FT THIOETH 1 18 ABU-S-CYS (METHYLLANTHIONINE).
 FT THIOETH 4 14 ALA-S-CYS (LANTHIONINE).
 FT THIOETH 5 11 ABU-S-CYS (METHYLLANTHIONINE).
 SQ SEQUENCE 19 AA: 2033 MW: F434299E2736286A CRC64 ;

Query Match 37.2%; Score 16; DB 1; Length 19;
 Best Local Similarity 50.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 3 FGSLAF 8
 1 1 1 : 8
 Db 7 FGPLIW 12

RESULT 24
 MDH_BREDI
 ID MDH_BREDI STANDARD; PRT; 19 AA.
 AC P8042;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE MALATE DEHYDROGENASE (EC 1.1.1.37) (FRAGMENT).
 GN
 OS Brevundimonas diminuta (Pseudomonas diminuta).
 OC Bacterium; Proteobacteria; alpha subdivision; Caulobacter group;
 OC
 RN [1]
 RP
 SEQUENCE.
 STRAIN=ATCC 11568;
 RX MEDLINE; 97334132.
 RA Charnock C.;
 RT "Structural studies of malate dehydrogenases (MDHs): MDHs in Brevundimonas species are the first reported MDHs in Proteobacteria which resemble lactate dehydrogenases in primary structure.";
 RT J. Bacteriol. 179:4066-4070(1997).
 CC -1- CATALYTIC ACTIVITY: L-MALATE + NAD(+) = OXALOACETATE + NADH.
 DR INTERPRO; IPR001252; -.
 DR PROSITE; PS00068; MDH; PARTIAL.
 KW Oxidoreductase; tricarboxylic acid cycle; NAD.
 FT NON_TER 19 19 MW: 3E643277AB542F23 CRC64 ;

OS Brevundimonas diminuta (Pseudomonas diminuta).
 OC Bacterium; Proteobacteria; alpha subdivision; Caulobacter group;
 OC
 RN [1]
 RP
 SEQUENCE.
 STRAIN=ATCC 11568;
 RX MEDLINE; 97334132.
 RA Charnock C.;
 RT "Structural studies of malate dehydrogenases (MDHs): MDHs in Brevundimonas species are the first reported MDHs in Proteobacteria which resemble lactate dehydrogenases in primary structure.";
 RT J. Bacteriol. 179:4066-4070(1997).
 CC -1- CATALYTIC ACTIVITY: L-MALATE + NAD(+) = OXALOACETATE + NADH.
 DR INTERPRO; IPR001252; -.
 DR PROSITE; PS00068; MDH; PARTIAL.
 KW Oxidoreductase; tricarboxylic acid cycle; NAD.
 FT NON_TER 19 19 MW: 3E643277AB542F23 CRC64 ;

OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
 OC Brevundimonas.
 RN [1]
 RP
 SEQUENCE.
 STRAIN=ATCC 11426;
 RX MEDLINE; 97334132.
 RA Charnock C.;
 RT "Structural studies of malate dehydrogenases (MDHs): MDHs in Brevundimonas species are the first reported MDHs in Proteobacteria which resemble lactate dehydrogenases in primary structure.";
 RT J. Bacteriol. 179:4066-4070(1997).
 CC -1- CATALYTIC ACTIVITY: L-MALATE + NAD(+) = OXALOACETATE + NADH.
 CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
 DR INTERPRO; IPR001252; -.
 DR PROSITE; PS00068; MDH; PARTIAL.
 KW Oxidoreductase; tricarboxylic acid cycle; NAD.
 FT NON_TER 19 19 MW: 3E643277AB542F23 CRC64 ;

Query Match 37.2%; Score 16; DB 1; Length 19;
 Best Local Similarity 66.7%; Pred. No. 2.8e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IFGSLA 7
 Db 13 IGGTLA 18

RESULT 25
 MDH_BREVE
 ID MDH_BREVE STANDARD; PRT; 19 AA.
 AC P80543;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE MALATE DEHYDROGENASE (EC 1.1.1.37) (FRAGMENT).
 GN
 OS Brevundimonas vesicularis (Pseudomonas vesicularis).

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 14, 2000, 11:56:53 : Search time 13.23 Seconds
(without alignments)
43.170 Million cell updates/sec

Title: US-09-277-074-10
Perfect score: 43
Sequence: 1 KIFGSLAFL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 3930

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0*
Maximum Match 100*

Listing first 45 summaries

Database : PIR_65.4*
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	60.5	17	PA0004	Plasocyanin - Ara
2	21	48.8	20	A60365	chymotrypsin inhib
3	21	48.8	20	A60365	trypsin inhibitor
4	20	46.5	16	A48839	T-cell receptor al
5	19	44.2	9	PT0225	19 heavy chain CDR
6	19	44.2	10	S06964	hypothetical prote
7	19	44.2	12	A37933	19 lambda chain J
8	19	44.2	14	B61597	cytochrome P450 AL
9	19	44.2	17	S71864	glutathione transf
10	19	44.2	17	S40530	aluronate protein -
11	19	44.2	17	PH1312	19 heavy chain DJ
12	19	44.2	18	JS0647	pheroconotropin -
13	19	44.2	20	PU0033	aldose 1 epimerase
14	18	41.9	11	A5594	buccalin - Califor
15	18	41.9	14	B39111	19 heavy chain V
16	18	41.9	14	A59018	MUC1 enhancer bind
17	18	41.9	15	PC4213	bpfB protein - Com
18	18	41.9	19	EWSMCN	cinnamycin - Strep
19	17	39.5	8	PC4373	telomeric and tetr
20	17	39.5	11	A57458	gene Gax protein -
21	17	39.5	12	S47393	T-cell antigen rec
22	17	39.5	15	PA0027	protein QA100006 -
23	17	39.5	15	PA0026	protein QA300027 -
24	17	39.5	15	B45115	peptidylprolyl iso
25	17	39.5	16	S24667	protein-tyrosine k
26	17	39.5	16	T14224	NADP dehydrogenase
27	17	39.5	17	S50901	chlorophyll a/b-bi
28	17	39.5	17	B42965	talin (glycosylate
29	17	39.5	17	T78870	gene Rbl protein -

ALIGNMENTS

RESULT 1						
PA0004	plasocyanin - Arabidopsis thaliana (fragment)					
C; Species: Arabidopsis thaliana (mouse-ear cress)						
C; Date: 18-Nov-1994 #sequence_revision 06-Jan-1995 #text_change 15-Mar-1996						
C; Accession: PA0004						
R; Kano, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.						
Submitted to JIPID, July 1994						
A; Description: Separation and characterization of <i>Arabidopsis</i> proteins by two-dimensi						
A; Reference number: PA0001						
A; Accession: PA0004						
A; Molecule type: protein						
A; Residues: 1-17 <XAM>						
A; Experimental source: stem						
C; Superfamily: plastocyanin						
C; Keywords: copper; electron transfer						
Query Match						
Best Local Similarity	60.5%	Score 26;	DB 2;	Length 17;		
Matches	5	Best Local Similarity	83.3%	Pred. No. 37;		
		Matches	1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	4	GSLAFL	9			
		Db	10 GSLAFL 15			
RESULT 2						
B60365	chymotrypsin inhibitor 2 - tobacco hornworm (fragment)					
C; Species: <i> Manduca sexta</i> (tobacco hornworm)						
C; Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 03-Feb-1994						
C; Accession: B60365						
R; Kano, M.R.						
Insect Biochem. 20, 141-147, 1990						
A; Title: Isolation and characterization of four serine proteinase inhibitors (serpins)						
A; Reference number: A60365						
A; Accession: B60365						
A; Molecule type: protein						
A; Residues: 1-20 <XAM>						
C; Keywords: hemolymph; monomer; serine proteinase inhibitor						
Query Match						
Best Local Similarity	48.8%	Score 21;	DB 2;	Length 20;		
Matches	4	Best Local Similarity	50.0%	Pred. No. 4.9e+02;		
		Matches	2;	Mismatches 2;	Indels 0;	Gaps 0;
QY	2	IFGSLAFL	9			
		Db	9 LHGSUYFI 16			

RESULT 3

Qy A60365 trypsin inhibitor - tobacco hornworm (fragment)

C:Species: Manduca sexta (tobacco hornworm)

C:Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 03-Feb-1994

C:Accession: A60365

R:Kanost, M.R.

Inset: Blochem, 20, 141-147, 1990

A:Title: Isolation and characterization of four serine proteinase inhibitors (serpins)

A:Reference number: A60365

A:Accession: A60365

A:Molecule type: protein

A:Residues: 1-20 <KAN>

C:Keywords: hemolymph; monomer; serine proteinase inhibitor

Query Match 48.8% Score 21; DB 2; Length 20;

Best Local Similarity 66.7% Pred. No. 4.9e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GSIAFL 9

Db 11 GILIAFI 16

RESULT 4

Qy A48839 T-cell receptor alpha chain V-N-J region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997

C:Accession: A48839

R:Ratz, J.D.; Wang, B.; Haskins, K.; Benoist, C.; Mathis, D.

Cell 74, 1089-1100, 1993

A:Title: Following a diabetogenic T cell from genesis through pathogenesis.

A:Reference number: A48839; MUID:94006520

A:Accession: A48839

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-16 <KAT>

A:Experimental source: NOD, transgenic, diabetogenic T cell clone BDC2.5

A:Note: sequence extracted from NCBI backbone (NCBIP:138465)

C:Keywords: T-cell receptor

Query Match 46.5% Score 20; DB 2; Length 16;

Best Local Similarity 100.0% Pred. No. 6.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IFGS 5

Db 12 IFGS 15

RESULT 5

Qy PT0225 Ig heavy chain CDR3 region (clone 1-103) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0225

R:Yamada, M.; Wasserman, R.; Richard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A:Reference number: PT0222; MUID:91108337

A:Accession: PT0225

A:Molecule type: DNA

A:Residues: 1-9 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match 44.2% Score 19; DB 2; Length 9;

Best Local Similarity 50.0% Pred. No. 1.8e+05;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IFGSLA 7

Db 2 MFGMMA 7

RESULT 6

Qy S06964 hypothetical protein (nifa 5' region) - Rhizobium leguminosarum (fragment)

C:Species: Rhizobium leguminosarum

C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 08-Oct-1999

C:Accession: S06964

R:Roelvink, P.W.; Hontelez, J.G.J.; van Kammen, A.; van den Bos, R.C.

Mol. Microbiol. 3, 1441-1447, 1989

A:Title: Nucleotide sequence of the regulatory nifa gene of Rhizobium leguminosarum P

A:Reference number: S06964

A:Accession: S06964

A:Molecule type: DNA

A:Residues: 1-10 <ROE>

A:Cross-references: EMBL:XI7073; NID:946208; PIDN:CAA34923.1; PID:9809748

Query Match 44.2% Score 19; DB 2; Length 10;

Best Local Similarity 66.7% Pred. No. 6.4e+02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 FGSLAF 8

Db 4 FGVLKF 9

RESULT 7

Qy A37933 Ig lambda chain J region - sheep (fragment)

C:Species: Ovis ammon aries, Ovis ammon aries (domestic sheep)

C:Date: 26-Jul-1991 #sequence_revision 26-Jul-1991 #text_change 05-Nov-1999

C:Accession: A37933

R:Reynard, C.A.; Mackay, C.R.; Mueller, R.G.; Weill, J.C.

Cell 64, 995-1005, 1991

A:Title: Somatic generation of diversity in a mammalian primary lymphoid organ: the sheep

A:Reference number: A37933; MUID:91160063

A:Accession: A37933

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-12 <REY>

A:Cross-references: GB:M60440; NID:9165946; PIDN:AAA31550.1; PID:9552425

C:Keywords: heterotetramer; immunoglobulin

Query Match 44.2% Score 19; DB 2; Length 12;

Best Local Similarity 75.0% Pred. No. 7.7e+02;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IFGS 5

Db 2 VFGS 5

RESULT 8

Qy B61597 cytochrome P450 AL-2 - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

C:Accession: B61597

R:Shimeno, H.; Toda, A.; Ogata, S.; Nagamatsu, A.

Drug Metab. Dispos. 19, 291-297, 1991

A:Title: Purification and aminoxygense activity of liver microsomal cytochrome P450 AL-2

A:Reference number: A61597; MUID:91232910

A:Accession: B61597

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-14 <SH1>

Query Match 44.2%; Score 19; DB 2; Length 14;
 Best Local Similarity 80.0%; Pred. No. 9e+02; Gaps 0;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SLAFL 9
 1:1:1
 Db 6 SLSFL 10

RESULT 9

SLAFL 9
 glutathione transferase (EC 2.5.1.18) class alpha 6a - pig (fragment)
 N: Alternative names: glutathione S-transferase class alpha 6a
 C: Species: Sus scrofa domestica (domestic pig)
 C: Accession: S71864 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
 R: Rouimi, P.; Anglade, P.; Debrauer, L.; Tulliez, J.
 Biochem. J. 317, 879-884, 1996
 A: Title: Characterization of pig liver glutathione S-transferases using HPLC-electrospray
 A: Reference number: S71864; MUID:96332484
 A: Accession: S71864
 A: Molecule type: protein
 A: Residues: 1-17 <ROU>
 A: Experimental source: liver; cytosolic
 C: Comment: At least five species-independent classes of cytosolic glutathion transferase mitochondrial form are known.
 C: Function: dimer
 A: Description: catalyzes the nucleophilic conjugation of intracellular glutathione to a
 A: Pathway: detoxification; xenobiotics metabolism
 A: Note: Increased hydrophilicity of GSH-conjugates facilitates their further metabolism
 C: Superfamily: glutathione transferase
 C: Keywords: dimer; transferase

Query Match 44.2%; Score 19; DB 2; Length 17;
 Best Local Similarity 80.0%; Pred. No. 1.1e+03; Gaps 0;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GSLAF 8
 1:1:1
 Db 2 GSLLF 6

RESULT 10

GSLAF 8
 aleurone protein - barley
 C: Species: Hordeum vulgare (barley)
 C: Accession: S40530 #sequence_revision 19-Mar-1997 #text_change 11-Jan-2000
 R: Yupsansis, T.; Burgess, S.R.; Jackson, P.J.; Shewry, P.R.
 J. Exp. Bot. 41, 385-392, 1990
 A: Title: Characterization of the major protein component from aleurome cells of barley
 A: Reference number: S40530
 A: Accession: S40530
 A: Status: preliminary
 A: Molecule type: protein
 A: Residues: 1-17 <YUP>
 C: Superfamily: glycinin

Query Match 44.2%; Score 19; DB 2; Length 17;
 Best Local Similarity 42.9%; Pred. No. 1.1e+03; Gaps 0;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IFGSLAFL 8
 1:1:1
 Db 11 VFGPRSF 17

RESULT 11

Qy 2 IFGSLSL 6
Db 7 VFFDQL 11

RESULT 14
A3594 buccalin - California sea hare
C.Species: *Aplysia californica* (California sea hare)
C.Date: 14-Sep-1990 #sequence_revision 14-Sep-1990 #text_change 24-Jun-1993
C;Accession: A35594
R;Crotter, E.C.; Miller, M.W.; Tenenbaum, R.; Kolks, M.A.G.; Kupfermann, I.; Weiss, K.R.
Proc. Natl. Acad. Sci. U.S.A. 85, 6177-6181, 1988
A;Title: Structure and action of buccalin, a modulatory neuropeptide localized to an ide
A;Reference number: A35594; MUID:88320404
A;Accession: A35594
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <CRO>

Query Match 41.9% Score 18; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIFGS 5
Db 3 QIYGS 7

RESULT 17
PC4213 bphB protein - *Comamonas testosteroni* (fragment)
C.Species: *Comamonas testosteroni*
C;Accession: PC4213
C;Date: 17-Dec-1996 #sequence_revision 21-Jan-1997 #text_change 08-Oct-1999
C;Accession: PC4213
C;Sylvestre, M.; Sirols, M.; Hurtubise, Y.; Bergeron, J.; Ahmad, D.; Shareck, F.; Bar
Gene 174, 195-202, 1996
A;Title: Sequencing of *Comamonas testosteroni* strain B-356-biphenyl/chlorobiphenyl di
A;Reference number: JC4993; MUID:97045812
A;Accession: PC4213
A;Molecule type: DNA
A;Residues: 1-15 <SYL>
A;Cross-references: GB:047637; NID:91245151; PIDN: AAC44530.1; PID:91245156
A;Experimental source: strain B-356
C;Genetics:
A;Gene: bphB

Query Match 41.9% Score 18; DB 2; Length 15;
Best Local Similarity 33.3%; Pred. No. 1.6e+03;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9
Db 2 KLTGEVALL 10

RESULT 18
EMSMCN cinnamycin - *Streptoverticillium cinnamoneum*
N;Alternate names: lanthiopeltin; lanthiobiotic Ro 09-0198
C.Species: *Streptoverticillium cinnamoneum*
C;Accession: A45767
C;Date: 30-Sep-1993 #sequence_revision 12-May-1994 #text_change 07-May-1999
C;Accession: A45767
R;Naruse, N.; Teruyo, O.; Tomita, K.; Konishi, M.; Miyaki, T.; Kawaguchi, H.; Fukase,
J. Antibiot. 42, 837-845, 1989
A;Title: Lanthiopeltin, a new peptide antibiotic. Production, isolation and propertie
A;Reference number: A45767; MUID:89221558
A;Accession: A45767
A;Molecule type: protein
A;Residues: 1-19 <NAR>
R;Wakamiya, T.; Fukase, K.; Naruse, N.; Konishi, M.; Shtba, T.
Tetrahedron Lett. 29, 4771-4772, 1988
A;Title: Lanthiopeltin, a new peptide effective against *Herpes simplex* virus: STRUCTU
A;Contents: annotation; strain L337-2
A;Reference number: A53359
C;Superfamily: cinnamycin precursor
C;Keywords: antibiotic; beta-hydroxyaspartic acid; lanthioline
F;1-18/Cross-link: (2S,3S,6R)-3-methyl-lanthioline (Cys-Thr) #status experimental
F;4-14/Cross-link: sn-(2S,6R)-3-methyl-lanthioline (Ser-Cys) #status experimental
F;5-11/Cross-link: (2S,3S,6R)-3-methyl-lanthioline (Cys-Thr) #status experimental
F;6-19/Cross-link: (2X1,9S)-lysinoalanine (Ser-Lys) #status experimental
F;15/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

Query Match 41.9% Score 18; DB 1; Length 19;
Best Local Similarity 42.9%; Pred. No. 2e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 FGSLAFL 9
Db 7 FGPFETV 13

RESULT 16
A59018 MUC1 enhancer binding protein 70K chain MUC1EBP-70 - human (fragment)
C.Species: Homo sapiens (man)
C.Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 08-May-1998
C;Accession: A59018
R;Abe, M.; Smith, C.J.; Larson, C.J.
A;Description: Involvement of "Ku-like" proteins in the transcription of MUC1/DE3, a bre
A;Reference number: A59018
A;Accession: A59018
A;Molecule type: protein
A;Residues: 1-14 <ABE>
A;Experimental source: breast cancer cell line MCF-7
A;Note: 3'-val was also found
C;Keywords: DNA binding; heterodimer

RESULT 19
 PC4373 telomeric and tetraplex DNA binding protein qTBPA2 III - rat (fragment)
 C;Species: *Rattus norvegicus* (Norway rat)
 C;Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 07-May-1999
 C;Accession: PC4373
 R;Sarig, G.; Weisman-Shomer, P.; Fry, M.
 A;Title: Telomeric and tetraplex DNA binding properties of qTBPA2: A homologue of the CTPase
 A;Reference number: PC4371; MUID:97445086
 A;Accession: PC4373
 A;Molecule type: protein
 A;Residues: 1-8 <SAR>
 A;Domain: RNPI #status predicted <RNP>
 C;Comment: This protein binds either strand of the telomeric DNA as well as unimolecular F1-4/Domain: RNPI #status predicted <RNP>

Query Match 39.5%; Score 17; DB 2; Length 12;
 Best Local Similarity 57.1%; Pred. No. 2e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 IFGSLAF 8
 Db 5 IVGTEAF 11

RESULT 22
 PA0027 protein QA100006 - Arabidopsis thaliana (fragment)
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
 C;Accession: PA0027
 R;Kano, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
 submitted to JIPID, July 1994
 A;Description: Separation and characterization of Arabidopsis proteins by two-dimensi
 A;Reference number: PA0001
 A;Accession: PA0027
 A;Molecule type: protein
 A;Residues: 1-15 <KAM>
 A;Experimental source: callus

Query Match 39.5%; Score 17; DB 2; Length 15;
 Best Local Similarity 50.0%; Pred. No. 2.5e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KIFG 4
 Db 3 KVYG 6

RESULT 23
 PA0026 protein QA300027 - Arabidopsis thaliana (fragment)
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
 C;Accession: PA0026
 R;Kano, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
 submitted to JIPID, July 1994
 A;Description: Separation and characterization of Arabidopsis proteins by two-dimensi
 A;Reference number: PA0001
 A;Accession: PA0026
 A;Molecule type: protein
 A;Residues: 1-15 <KAM>
 A;Experimental source: leaf

Query Match 39.5%; Score 17; DB 2; Length 15;
 Best Local Similarity 50.0%; Pred. No. 2.5e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KIFG 4
 Db 3 KVYG 6

RESULT 24
 B45115 peptidylprolyl isomerase (EC 5.2.1.8) FKBP51 - human (fragment)
 N;Alternate names: FK506-binding protein FKBP51; peptidylprolyl cis-trans isomerase F
 C;Species: Homo sapiens (man)
 C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
 C;Accession: B45115
 R;Wlederrecht, G.; Hung, S.; Chan, H.K.; Marcy, A.; Martin, M.; Calaycay, J.; Boulton
 J. Biol. Chem. 267, 21753-21760, 1992
 A;Title: Characterization of high molecular weight FK-506 binding activities reveals
 A;Reference number: A45115; MUID:93016131

RESULT 21
 S47393 T-cell antigen receptor VJ junction beta chain - human
 C;Species: Homo sapiens (man)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C;Accession: S47393
 R;Lehner, P.J.
 Submitted to the EMBL Data Library, August 1994
 A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
 A;Reference number: S47393
 A;Accession: S47393
 A;Title: Preliminary
 A;Molecule type: mRNA
 A;Residues: 1-12 <LEH>
 A;Cross-references: EMBL:Z35670; PID:9527445; PID:CAA84739.1; PID:9527446
 A;Reference number: A45115; MUID:93016131

A;Accession: B45115
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-15 <WIE>
 A;Experimental source: JURKAT cells
 A;Note: sequence extracted from NCBI backbone (NCBIP:116748)
 C;Keywords: cis-trans-isomerase; cyclosporin A binding

Query Match 39.5% Score 17; DB 2; Length 15;
 Best Local Similarity 60.0%; Pred. No. 2.5e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 SLAFL 9
 |:|:
 Db 4 SIAVL 8

RESULT 25
 S24667
 protein-tyrosine kinase (EC 2.7.1.112) kit - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 03-Mar-1994 #sequence_revision 13-Mar-1997 #text_change 04-Feb-2000
 C;Accession: S24667
 R;Sorrentino, V.
 Submitted to the EMBL Data Library, May 1992
 A;Reference number: S24666
 A;Accession: S24667
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-16 <SOR>
 A;Cross-references: EMBL:X65998; NID:950433; PID:CNA46799.1; PID:950434
 C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

Query Match 39.5% Score 17; DB 2; Length 16;
 Best Local Similarity 60.0%; Pred. No. 2.7e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 SLAFL 9
 |:||:
 Db 8 AMAFL 12

Search completed: November 14, 2000, 11:58:05
 Job time: 72 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 14, 2000, 11:56:53 ; Search time 17.04 Seconds
(without alignments)

49.317 Million cell updates/sec

Title: US-09-277-074-10
Perfect score: 43
Sequence: 1 KIFGSLAFL 9

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 4186

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%, Maximum Match 100%
Listing first 45 summaries

Database : SPTRMBL14:*

```

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_minc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodont:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	DB	ID	Description
1	25	58.1	18	2	Q9RQ90	Q9RQ90 buchnera ap
2	22	51.2	18	2	Q06514	Q06514 escherichia
3	22	51.2	20	2	Q9RA11	Q9RA11 bordetella
4	21	48.8	16	13	P82391	P82391 litoria aur
5	20	46.5	15	11	Q9R0X7	Q9R0X7 mus musculus
6	20	46.5	16	13	P82388	P82388 litoria aur
7	20	46.5	16	13	P82389	P82389 litoria aur
8	20	46.5	16	13	P82392	P82392 litoria aur
9	20	46.5	20	2	Q32710	Q32710 klebsiella
10	19	44.2	10	2	Q52837	Q52837 rhizobium l
11	19	44.2	18	6	Q95305	Q95305 sus scrofa
12	19	44.2	18	13	P82068	P82068 litoria gen
13	18	41.9	10	10	Q9QKJ0	Q9QKJ0 human immun
14	18	41.9	12	12	Q89243	Q89243 woodchuck h
15	18	41.9	15	8	Q9T2G9	Q9T2G9 solanum tub
16	18	41.9	16	10	Q82403	Q82403 fragaria ve
17	18	41.9	16	13	P82390	P82390 litoria aur
18	18	41.9	17	5	Q26832	Q26832 trypanosoma
19	18	41.9	17	5	Q9VVG5	Q9VVG5 drosophila

ALIGNMENTS

RESULT	1	Preliminary; PRT; 18 AA.					
ID	Q9RQ90	AC	Q9RQ90;				
DT	01-MAY-2000	(TREMBLrel.	13, Created)				
DT	01-MAY-2000	(TREMBLrel.	13, Last sequence update)				
DT	01-MAY-2000	(TREMBLrel.	13, Last annotation update)				
DE	HYPOTHETICAL 1.9 KDA PROTEIN (FRAGMENT).						
OS	Buchnera aphidicola.						
OC	Bacteria; Proteobacteria; gamma subdivision; Buchnera.						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RX	MEDLINE: 20022390.						
RA	Clark M.A., Moran N.A., Baumann P.;						
RT	*Sequence evolution in bacterial endosymbionts having extreme base						
RT	compositions.;						
RL	Mol. Biol. Evol. 16:1586-1598(1999).						
DR	EMBL; AF122281; AAF13768.1; -.						
KW	Hypothetical protein.						
FT	NON_TER	1	1				
SQ	SEQUENCE	18	AA:	1885	MW:	96F90072D88F4425 CRC64:	

Query	Match	Score	25;	DB	2;	Length	18;
Best	Local Similarity	100.0%	Pred. No.	1.4e-02;			
Matches	5;	Conservative	0;	Mismatches	0;	Indels	0;
QY	1	KIFGS	5				
Db	3	KIFGS	7				
RESULT	2						
ID	Q06514	AC	Q06514;	PRELIMINARY;			
DT	01-JUL-1997	(TREMBLrel.	04, Created)				
DT	01-JUL-1997	(TREMBLrel.	04, Last sequence update)				
DR	01-JUL-1997 (TREMBLrel.	04, Last annotation update)					
DE	DNA, MOSAIC MERCURY RESISTANCE TRANSPORTABLE ELEMENT						
DE	(MER-OPERON)1040 BP (FRAGMENT).						
GN	MER.						

OS	Escherichia coli.	RT	bell frogs <i>Litoria aurea</i> and <i>Litoria raniformis</i> .;
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;	RL	Eur. J. Biochem. 0:0-0(2000).
OC	Escherichia.	CC	-!- FUNCTION: AUREIN 2.4 HAS ANTIMICROBIAL AND ANTICANCER ACTIVITY.
RN	[1]	KW	
RP	SEQUENCE FROM N.A.	Antibiotic	
RC	STRAIN=CH210; TRANSPONSON=TNS0559;	PEPTIDE	3
RX		FT	16
RA	NIKIFOROV V., Kholodii G., Minakhin L., Gorlenko Z., Kalyaeva E.,	MOD_RES	16
RA	Mindlin S., Nikiforov V.,	SEQUENCE	16 AA;
RA	"Intercontinental spread of promiscuous mercury-resistance transposons in environmental bacteria,"		1630 MW;
RL	Mol. Microbiol. 24:321-329 (1997).		1DB7980438AAE2F9 CRC64;
DR	EMBL: Y09026; CNA70241.1; .		
FT	NON_TER 18		
SQ	SEQUENCE 18 AA; 1899 MW; 484AA2D7197814DF9 CRC64;		
Query Match	Score 51.2%; Best Local Similarity 57.1%; Matches 4;	Score 22; DB 2; Length 18; Pred. No. 5.7e+02; 2; Conservative	RESULT 5
Qy	1 KIFGSLAFL 7	Indels 0; Gaps 0;	Q9R0X7 PRELIMINARY; PRT; 15 AA.
Db	1 : 1 : 1		Q9R0X7 ID
	3 KIFGSLAFL 9		AC 09R0X7: 13, Created)
			DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
			DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
			DE ACTIVATED NOTCH1 ONCOPROTEIN (FRAGMENT).
			GN NOTCH1.
			OS Mus musculus (Mouse).
			OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
			OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
			RN [1]
			RP SEQUENCE FROM N.A.
			RA Lee J.S., Ishimoto A., Yanagawa S. i.;
			RT "Murine leukemia provirus-mediated activation of the Notch1 gene leads to induction of HES-1 in a mouse T lymphoma cell line, DL-3.;"
			RL FEBS Lett. 455:276-280(1999).
			DR EMBL: AJ238029; CAB40733.1; .
			FT NON_TER 15
			SQ SEQUENCE 15 AA; 1794 MW; C06FC27C9B6E307B CRC64;
Query Match	Score 51.2%; Best Local Similarity 55.6%; Matches 5;	Score 22; DB 2; Length 20; Pred. No. 6.3e+02; 1; Conservative	RESULT 6
Qy	1 KIFGSLAFL 9	Indels 0; Gaps 0;	P82388 PRELIMINARY; PRT; 16 AA.
Db	1 : 1 : 1		ID P82388
	8 RIDGAAFL 16		AC P82388;
			DT 01-MAY-2000 (TrEMBLrel. 13, Created)
			DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
			DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
			DE AUREIN 2.1/2.1.1.
			OS Litoria raniformis, and <i>Litoria aurea</i> (Australian frog).
			OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
			OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hyldidae;
			OC Litoria.
			RN [1]
			RP SEQUENCE
			RA Rozek T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A., Wallace J.C., Tyler M.J.,
			RA "The antibiotic and anticancer aurein peptides from the Australian bell frogs <i>Litoria aurea</i> and <i>Litoria raniformis</i> .;"
			RL Eur. J. Biochem. 0:0-0(2000).
			CC -!- FUNCTION: AUREIN 2.1 HAS ANTIMICROBIAL AND ANTICANCER ACTIVITY.
			KW Amidation; Antibiotic
			FT PEPTIDE 3 16
			MOD_RES 16 16 AMIDATION.

The antibiotic and anticancer aurein peptides from the Australian

Rozek T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A.,

Wallace J.C., Tyler M.J.,

"The antibiotic and anticancer aurein peptides from the Australian

SQ	SEQUENCE	16 AA;	1616 MW;	1D9A5DADB4D240F9	CRC64;	Best Local Similarity 100.0%; Pred. No. 1.3e+03; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Query Match	46.5%; Score 20; DB 13; Length 16;					
Best Local Similarity 100.0%; Pred. No. 1.3e+03; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	3 FGSL 6					
Db	13 FGSL 16					
RESULT 7						
P82389	PRELIMINARY;	PRT;	16 AA.			
ID	P82389;					
AC						
DT	01-MAY-2000 (TREMBLrel. 13, Created)					
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)					
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)					
DE	AUREIN 2.2/2.2.1.					
OS	Litoria aurea (Australian frog).					
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
CC	Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;					
CC	Litoria.					
RP	SEQUENCE.					
RA	Rozek T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A.,					
RA	Wallace J.C., Tyler M.J.,					
RT	"The antibiotic and anticancer aurein peptides from the Australian bell frogs Litoria aurea and Litoria raniformis."					
RL	Eur. J. Biochem. 0:0 (2000).					
CC	-1- FUNCTION: AUREIN 2.2 HAS ANTIMICROBIAL AND ANTICANCER ACTIVITY.					
KW	Amidation; Antibiotic.					
FT	PEPTIDE 3 16 AMIDATION.					
MOD_RES	16 16 AMIDATION.					
SQ	SEQUENCE 16 AA; 1616 MW; 1D9A5DADB4D240F9	CRC64;				
Query Match	46.5%; Score 20; DB 13; Length 16;					
Best Local Similarity 44.4%; Pred. No. 1.3e+03; Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;						
Qy	1 KIGSGAFL 9					
Db	1 KIGSGAFL 16					
RESULT 8						
P82392	PRELIMINARY;	PRT;	16 AA.			
ID	P82392;					
AC	P82392;					
DT	01-MAY-2000 (TREMBLrel. 13, Created)					
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)					
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)					
DE	AUREIN 2.5.					
OS	Litoria raniformis, and Litoria aurea (Australian frog).					
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
CC	Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;					
CC	Litoria.					
RP	SEQUENCE.					
RA	Rozek T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A.,					
RA	Wallace J.C., Tyler M.J.,					
RT	"The antibiotic and anticancer aurein peptides from the Australian bell frogs Litoria aurea and Litoria raniformis."					
RL	Eur. J. Biochem. 0:0 (2000).					
CC	-1- FUNCTION: HAS ANTIMICROBIAL AND ANTICANCER ACTIVITY.					
KW	Amidation; Antibiotic.					
FT	MOD_RES 16 16 AMIDATION.					
SQ	SEQUENCE 16 AA; 1650 MW; 1D9A5DADB4D240F9	CRC64;				
Query Match	46.5%; Score 20; DB 13; Length 16;					
Best Local Similarity 44.2%; Pred. No. 1.3e+03; Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;						
Qy	3 FGSLAF 8					

Db 4 FGVLKF 9
 RESULT 11
 Q95305 PRELIMINARY; PRT; 18 AA.
 ID Q95305; AC P82068; PRELIMINARY; PRT; 18 AA.
 AC P82068; PRELIMINARY; PRT; 18 AA.
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DE MITOCHONDRIAL PHOSPHATE CARRIER PROTEIN (FRAGMENT).
 OS Sus scrofa (pig).
 OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE-SMALL INTESTINE;
 RA Wintero A.K.; Fredholm M.; Davies W.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Z81168; CAB03553.1; -.
 KW Mitochondrion.
 FT NON_TER 18 AA; 1985 MW; 07DBDAC362B0ACD4 CRC64;
 SQ SEQUENCE 18 AA; 1985 MW; 07DBDAC362B0ACD4 CRC64;

Query Match 44.2%; Score 19; DB 6; Length 18;
 Best Local Similarity 50.0%; Pred. No. 2.3e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 IFGSLAFL 9
 :|:|:|
 Db 1 MFESSVAIL 8

RESULT 12
 P82068 PRELIMINARY; PRT; 18 AA.
 ID P82068; AC P82068; PRELIMINARY; PRT; 18 AA.
 AC P82068; PRELIMINARY; PRT; 18 AA.
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE MACULATIN 2.1.
 OC Litoria genimaculata (Green-eyed tree frog).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Litoria.
 RN 11
 RP SEQUENCE, AND MASS SPECTROMETRY .
 RA Rozen T., Waugh R.J., Steinborner S.T., Bowie J.H., Tyler M.J.,
 Wallace J.C.;
 RT "The maculatin peptide from the skin glands of the tree frog
 Litoria genimaculata. A comparison of the structures and
 antibacterial activities of maculatin 1.1 and caerin 1.1.";
 RL J. Pept. Sci. 4:111-115(1998).
 CC -1- FUNCTION: SHOWS ANTI-BACTERIAL ACTIVITY AGAINST B.CERUSUS,
 L. INNOCUUS, M. LUTEUS, S. AUREUS, S. EPIDERMIS AND S. UBERIS.
 CC -1- TISSUE SPECIFICITY: SECRETED BY "THE SKIN DORSAL GLANDS".
 CC -1- MASS SPECTROMETRY: MW=1878; METHOD=FAB.
 KW Amphibian skin; Amidation; Antibiotic.
 FT MOD_RES 18 18 AMIDATION.
 SQ SEQUENCE 18 AA; 1879 MW; 9BA1F86BB4FACB8E CRC64;

Query Match 44.2%; Score 19; DB 13; Length 18;
 Best Local Similarity 42.9%; Pred. No. 2.3e+03;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 4 FGVLKF 9
 RESULT 13
 Qy 1 KIFGSLA 7
 :|:|:
 Db 8 KWAGFIA 14

Q90KJ0 PRELIMINARY; PRT; 10 AA.
 ID Q90KJ0; AC Q90KJ0; PRELIMINARY; PRT; 10 AA.
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviridae; Lentivirus.
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=22202V3.1;
 RA Kober B., Van Dyke R., Wolinsky S., Popak E., Macken C., Widmayer S., Viscarelio R.;
 RA Barduguez A., Hansen C., Wiznia A., Luzuriaga K.; Viscarelio R.;
 RA "The Ariel project: a prospective cohort study of maternal-child transmission of human immunodeficiency virus type 1 in the era of maternal antiretroviral therapy.";
 RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RL DR EMBL; AFI12548; AAF13326.1; -.
 KW Envelope Protein.
 FT NON_TER 10 AA; 961 MW; 4EDD23640DDB1DD7 CRC64;
 SQ SEQUENCE 10 AA; 961 MW; 4EDD23640DDB1DD7 CRC64;

Query Match 41.9%; Score 18; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GSLA 7
 ||||
 Db 1 GSLA 4

RESULT 14
 Q89243 PRELIMINARY; PRT; 12 AA.
 ID Q89243; AC Q89243; PRELIMINARY; PRT; 12 AA.
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DE CORE PROTEIN (FRAGMENT).
 OC Woodchuck hepatitis B virus.
 OC Viruses; Retroviridae; Hepadnaviridae; Orthohepadnavirus.
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=W64;
 RX MEDLINE; 87219879.
 RA Ettemble J., Moroy T., Trepo C., Tiollais P., Buendia M.A.;
 RT "Nucleotide sequence of the woodchuck hepatitis virus surface antigen mRNAs and the variability of three overlapping viral genes.";
 RL Gene 500:207-214(1986).
 DR EMBL: M15954; AAA69576.1; -.
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1388 MW; 21ABC172F2132B47 CRC64;

Query Match 41.9%; Score 18; DB 12; Length 12;
 Best Local Similarity 80.0%; Pred. No. 2.4e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIFGS 5
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 Db 7 KFGS 11

Q9T2G9 PRELIMINARY; PRT; 15 AA.
 ID Q9T2G9; AC Q9T2G9; PRELIMINARY; PRT; 15 AA.
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)

RESULT 15

DE	CARBONIC ANHYDRASE (EC 4.2.1.1) (FRAGMENT).	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OS	Solanum tuberosum (Potato).	OC	Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;	
OG	Chloroplast.	OC	Litoria.	
OC		RN	[1]	
OC		RP	SEQUENCE.	
OC		RA	Rozek T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A., Wallace J.C., Tyler M.J.;	
RN		RA	"The antibiotic and anticancer aurein peptides from the Australian bell frogs <i>Litoria aurea</i> and <i>Litoria raniformis</i> ."	
RP		RT	bell frogs Litoria aurea and Litoria raniformis.;	
RX	MEDLINE; 96327808.	RT	RL Eur J Biochem. 0-0-2000).	
RA	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Asteridae; euasterids I; Solanales; Solanaeae; Solanum.	CC	-1- FUNCTION: HAS ANTIMICROBIAL AND ANTICANCER ACTIVITY.	
OC		RT	L. leaves: characterization of two compartment-specific isoforms."	
RN		RT	Plantae 199:79-88 (1996).	
RP		RT	Amidation; Antibiotic.	
RX	SEQUENCE 15 AA; 1647 MW; CA5B7063CDD32976 CRC64;	FT	MOD_RES 16 AMIDATION.	
SQ		FT	SEQUENCE 16 AA; 1616 MW; 1D95DA424DAE2F9 CRC64;	
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Query Match	41.9%; Score 18; DB 8; Length 15;	Query Match	41.9%; Score 18; DB 13; Length 16;	
Best Local Similarity	80.0%; Pred. No. 3e+03;	Best Local Similarity	33.3%; Pred. No. 3.2e+03;	
Matches	0; Mismatches 1; Indels 0; Gaps 0;	Matches	3; Mismatches 3; Indels 0; Gaps 0;	
Qy	4 GSLAF 8	Qy	1 KIFGSLAFL 9	
Db	4 GSKAFA 8	Db	8 KVYGAIGSL 16	
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RESULT	16	RESULT	18	
082403	PRELIMINARY: PRT; 16 AA.	Q26632	PRELIMINARY; PRT; 17 AA.	
ID	082403;	ID	Q26632	
AC	082403;	AC	Q26632;1996 (TREMBLrel. 01, Created)	
DT	01-NOV-1998 (TREMBLrel. 08, Created)	DT	01-NOV-1998 (TREMBLrel. 01, Last sequence update)	
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)	DT	01-NOV-1998 (TREMBLrel. 08, Last annotation update)	
DE	01-NOV-1998 (TREMBLrel. 08, Last annotation update)	DE	(IATAF 1.2) VARIANT SURFACE GLYCOPROTEIN ELC GENE (FRAGMENT).	
DE	ALCOHOL DEHYDROGENASE (EC 1.1.1.1) (ALDEHYDE REDUCTASE) (FRAGMENT).	OS	Trypanosoma brucei brucei.	
GN	ADH.	OC	Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.	
OS	Fragaria vesca	RN	1.1.1	
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Rosidae; eurosids I; Rosales; Rosaceae; Fragaria.	RP	SEQUENCE FROM N.A.		
OC		RX	MEDLINE; 86228091.	
OC		RA	Brown K.H., Brentano S.T., Donelson J.E.;	
RN		RT	"Mung bean nuclease cleaves preferentially at the boundaries of STRAIN="PAWTUCKAWAY" sequences in trypanosome DNA."	
RP		RT	variant surface glycoprotein gene transpositions in trypanosome DNA."	
RC	SEQUENCE FROM N.A.	RL	J. Biol. Chem. 261:10352-10358 (1986).	
STRAIN="PAWTUCKAWAY";	YU H., Davis T.M.;	DR	EMBL; M14020; AAA30305 1; -.	
RA	*Genetic relations among <i>Fragaria</i> species based on RAPDs and an alcohol dehydrogenase (ADH) gene.";	FT	NON-TER 1	
RT	alcohol dehydrogenase (ADH) gene.";	FT	SEQUENCE 17 AA; 1973 MW; 9E00FB261B8FBFB CRC64;	
Genome 0.0-0(1997).	RL	SQ		
CC	-1- CATALYTIC ACTIVITY: AN ALCOHOL + NAD(+) = AN ALDEHYDE OR KETONE + NADH.	Query Match	41.9%; Score 18; DB 5; Length 17;	
CC	-1- COFACTOR: ZINC OR IRON.	Best Local Similarity	100.0%; Pred. No. 3.4e+03;	
DR	DAF00215; AAC36542.1; -.	Matches	0; Mismatches 0; Indels 0; Gaps 0;	
OXIDOREDUCTASE.		Qy	6 LAFL 9	
FT		Db	12 LAFL 15	
NON-TER	1	<hr/>		
FT	16 AA; 1666 MW; CEF73B5B28A4CA87 CRC64;	RESULT	19	
SQ		ID	Q9VVG5	
SEQUENCE 16 AA;		AC	Q9VVG5;	
		DT	01-MAY-2000 (TREMBLrel. 13, Created)	
		DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
		DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)	
		DE	CG7610 PROTEIN.	
		GN	CG7630.	
		OS	Drosophila melanogaster (Fruit fly).	
		OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
		OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
		OC	Ephydriidae; Drosophilidae; Drosophila.	
		RN	[1]	
		RP	SEQUENCE FROM N.A.	
		RC	STRAIN-BERKELEY;	
		RX	MEDLINE; 20196006.	
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RESULT	17			
P82390	PRELIMINARY;	PRT;	16 AA.	
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AC	:			
P82390;	8 RIFG 11			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)			
DE	AUREIN 2.3.			
OS	Litoria aurea (Australian frog).			

RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,	KW	Amidation; Antibiotic.
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,	FT	AUREIN 3.1.1.
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,	FT	AUREIN 3.1.2.
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,	FT	AMIDATION.
RA	Brandon R.C., Rogers Y.H.C., Blazquez R.G., Champine J., Pfeiffer B.D.,	FT	F6AC17930428EAFD CRC64 ;
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mikics G.I.G.,	SEQUENCE	17 AA; 1739 MW;
RA	Abril J.F., Aghayani A., An H.-J., Andrews-Pflanck C., Baldwin D.,	Query Match	Score 18; DB 13; Length 17;
RA	Ballew M.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,	Best Local Similarity	57.18; Pred. No. 3.4e+03;
RA	Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bochkov S.,	Matches	1; Mismatches 2; Indels 0; Gaps 0;
RA	Borkova D., Botchan M.R., Bouck J., Broststein P., Brottier P.,	4	
RA	Burtis K.C., Busam D.A., Butlire H., Cadieu E., Center A., Chandra I.,	Conservative	
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,	1	
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,	KIFGSLA 7	
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,	1	
RA	Durbin K.J., Evangelista C.C., Ferraz S., Ferreira S., Fleischmann W.,	Db	8 KIAGHIA 14
RA	Foster C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,		
RA	Glodek A., Gong F., Gorrell J.H., Guan P., Harris M.,	RESULT	21
RA	Harris N.J., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,	P82395	PRELIMINARY;
RA	Houston D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,	ID	P82395
RA	Jalil M., Kalush F., Karpen K.G.H., Kennison J.A., Ketchum K.A.,	AC	P82395;
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,	DT	01-MAY-2000 (TREMBLrel. 13, Created)
RA	Lasko P., Lei Y., Levitsky A.P., Li J., Li Z., Liang Y., Lin X.,	DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,	DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)
RA	Merkulov G., Milshina N.V., McBarry C., Morris J., Moskrefi A.,	DE	AUREIN 3.2.
RA	Mount S.M., Moy M., Murphy B., Murphy L., Mizny D.M., Nelson D.L.,	OS	Litoria raniformis, and Litoria aurea (Australian frog).
RA	Nelson D.R., Nissen K.A., Nixon K., Nusskern D.R., Paclib J.M.,	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puris M., Reese M.G.,	OC	Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,	OC	Litoria
RA	Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,	RN	[1]
RA	Spler E., Spredling A.C., Stapleton M., Strong R., Sun E.,	RP	SEQUENCE.
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,	RA	Rozek T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A.,
RA	Wang Z.-Y., Wassall M.A., Weissenbach J.,	RA	Wallace J.C., Tyler M.J.;
RA	Williams S.M., Woodward T., Worley K.C., Wu D., Weissbach J.,	RT	"The antibiotic and anticancer aurein peptides from the Australian
RA	Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,	RT	bell frogs Litoria aurea and Litoria raniformis.";
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,	RL	Bur. J. Biochem. 0:0 (2000).
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;	CC	-1; FUNCTION: HAS ANTIMICROBIAL AND ANTICANCER ACTIVITY.
RA	"The genome sequence of Drosophila melanogaster.";	KW	AMIDATION.
DR	EMBL: AE003524; AA149346.1; -.	FT	MOD.RES 17 17
DR	SCIENCE 287:2185-2195 (2000).	SEQUENCE	17 AA; 1769 MW; F6AC0A380428EAFD CRC64 ;
SQ	SEQUENCE 17 AA; 1865 MW; F982197C175EEBBA CRC64 ;		
RA	SEQUENCE 41.9%; score 18; DB 5; Length 17;	Query Match	Score 18; DB 13; Length 17;
RA	Best Local Similarity 100.0%; Pred. No. 3.4e+03;	Best Local Similarity	57.18; Pred. No. 3.4e+03;
RA	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches	1; Mismatches 2; Indels 0; Gaps 0;
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RA	5 SLAF 8	Db	8 KIAGHIA 14
RA		RESULT	22
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RA	ID	097668	
RA	AC	097668;	
RA	DT	01-MAY-1999 (TREMBLrel. 10, Created)	
RA	DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)	
RA	DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)	
RA	DE	LACTOBERRIN (FRAGMENT).	
RA	OS	EQUUS CABALLUS (Horse).	
RA	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
RA	OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.	
RA	RN	SEQUENCE FROM N.A.	
RA	RA	Brandon R.B., Giffard J.M., Belli T.K.;	
RA	RN	"Isolation of Equine Lactoferrin Gene."	
RA	RP	Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases	
RA	RA	EMBL; AF104025; AAC77463.1;	
RA	RA	HSSP; P24627; 1BLF.	
RA	RT	INTERPRO; IPR001156;	
RA	RT	PF00405; transferrin; 1.	
RA	RT	NON_TER 1	
RA	RT	NON_TER 18 18	
RA	SEQUENCE	18 AA; 1936 MW; D8FBFA226AA6DD9 CRC64 ;	
RA	RA	CC	
RA	Rozek T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A.,		
RA	RA	Wallace J.C., Tyler M.J.;	
RA	RT	"The antibiotic and anticancer aurein peptides from the Australian	
RA	RA	bell frogs Litoria aurea and Litoria raniformis.";	
RA	RA	Bur. J. Biochem. 0:0 (2000).	
RA	RT	-1; FUNCTION: AUREIN 3.1.1 IS NOT AMIDATED.	
RA	RA	-1; MISCELLANEOUS: AUREIN 3.1.1 IS NOT AMIDATED.	

Query Match	Best Local Similarity	Score	Length	Db	Db	Db
Matches 3;	Conservative	41.9%;	DB 6;03;	RESULT 25	12	GLLAF 16
Matches 2;		Pred. No. 3.6e+03;	Length 18;	Q73129	PRELIMINARY;	PRT;
		2; Mismatches	Indels 0;	AC Q73129;		19 AA.
Qy 4	GSLAFL 9	PRELIMINARY;	PRT;	AC Q73129;		
	1 : :			DT 01-NOV-1996 (TREMBLrel. 01, Created)		
Db 7	GDVAEV 12			DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)		
				DT 01-NOV-1996 (TREMBLrel. 01, Last annotation update)		
RESULT 23				DE ENVELOPE GLYCOPROTEIN (FRAGMENT).		
Q9T2G8				GN ENV.		
ID Q9T2G8				OS Human immunodeficiency virus type 1.		
AC Q9T2G8;				OC Viruses; Retroviroidea; Lentiviridae; Lentivirus.		
DT 01-MAY-2000 (TREMBLrel. 13, Created)				RN [1]		
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)				RP SEQUENCE FROM N.A.		
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)				RC STRAIN=SAMPLE P4.25-15;		
DE CARBONIC ANHYDRASE (EC 4.2.1.1) (FRAGMENT).				RA Wolinsky S.M., Korber B.T.M., Neumann A.J.U., Daniels M., Kunstman K.J., Whetsell A.J., Cao Y., Ho D.D., Safrit J.T., Roup R.A.;		
OS Solanum tuberosum (Potato).				RL Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.		
OC Chloroplast.				RN [2]		
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;				RP SEQUENCE FROM N.A.		
OC Magnoliophyta; eudicotyledons; Asteridae; euasterids I; Solanales;				RC STRAIN=SAMPLE P4.25-15;		
OC Solanaeae; Solanum.				RA McDonald D.; Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.		
RN [1]				RL DR EMBL; U36027; AAA97722.1; -.		
RP SEQUENCE.				KW Envelope protein.		
RX 96327808.				FT NON_TER 1 1		
RA Rumeau D., Cuine S., Fina L., Gault N., Nicole M., Peltier G.;				SQ SEQUENCE 19 AA; 2066 MW; E117102D528000EF4 CRC64;		
RT "Subcellular distribution of carbonic anhydrase in Solanum tuberosum				Query Match Best Local Similarity 41.9%; Score 18; DB 12; Length 19;		
RT L. leaves: characterization of two compartment-specific isoforms.";				Matches 4; Conservative 100.0%; Pred. No. 3.8e+03; Mismatches 0; Indels 0; Gaps		
RL Plantae 199:79-98(1996).				Qy 4 GSLA 7		
SEQUENCE 18 AA; 2017 MW;				Db 1 GSLA 4		
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Db 7 GSKAF 11						
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AC Q9UMM9;						
DT 01-MAY-2000 (TREMBLrel. 13, Created)						
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)						
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)						
DE ARGININE VASOPRESSIN-NEUROPHYSIN II (FRAGMENT).						
AVP.						
OS Homo sapiens (Human).						
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.						
RN [1]						
RP SEQUENCE FROM N.A.						
RA Ito M., Mori Y., Oiso Y., Saito H.;						
RT "A single base substitution in the coding region for neurophysin II associated with familial central diabetes insipidus.";						
RT J. Clin. Invest. 87:725-728(1991).						
RL EMBL; M63733; AAA69844.1; -.						
DR NON_TER 19 19						
FT SEQUENCE 19 AA; 1985 MW; 5FF5PCD7BD990451 CRC64;						
Query Match	41.9%;	Score 18;	DB 4;	Length 19;		
Best Local Similarity	80.0%;	Pred. No. 3.8e+03;	Length 18;			
Matches 4;	Conservative 0;	Mismatches 1;	Indels 0;			
Qy 4 GSLAF 8						

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OM protein - protein search, using sw model

Run on: November 14, 2000, 11:56:53 ; Search time 12.04 Seconds
(without alignments)
12.529 Million cell updates/sec

Title: US-09-277-074-10
Perfect score: 43
Sequence: 1 KIFGSLAFL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 1676186 residues

Total number of hits satisfying chosen parameters: 87906

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

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2: /cgtn2_6/ptodata/2/1aa/5B_COMB.pep:*

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4: /cgtn2_6/ptodata/2/1aa/PCU5_COMB.pep:*

5: /cgtn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	9	1 US-09-467-083-27	Sequence 70, App1
2	43	100.0	9	1 US-09-787-547-10	Sequence 27, App1
3	43	100.0	9	1 US-08-414-417B-27	Sequence 27, App1
4	43	100.0	9	2 US-08-486-448A-27	Sequence 27, App1
5	43	100.0	9	2 US-08-468-445B-27	Sequence 27, App1
6	43	100.0	9	2 US-08-902-516-18	Sequence 18, App1
7	43	100.0	9	4 PCT-US95-16415-10	Sequence 27, App1
8	43	100.0	9	4 US-08-466-580B-27	Sequence 10, App1
9	43	100.0	16	1 US-08-467-083-62	Sequence 62, App1
10	43	100.0	16	1 US-08-414-417B-22	Sequence 62, App1
11	43	100.0	16	2 US-08-486-348A-62	Sequence 62, App1
12	43	100.0	16	2 US-08-468-545B-62	Sequence 62, App1
13	43	100.0	16	2 US-08-466-580B-27	Sequence 62, App1
14	29	67.4	15	1 US-08-467-083-36	Sequence 36, App1
15	29	67.4	15	1 US-08-414-417B-36	Sequence 36, App1
16	29	67.4	15	2 US-08-486-448A-16	Sequence 36, App1
17	29	67.4	15	2 US-08-468-545B-36	Sequence 36, App1
18	29	67.4	15	3 US-08-468-545B-36	Sequence 36, App1
19	24	55.8	9	1 US-08-215-805A-11	Sequence 11, App1
20	24	55.8	15	1 US-08-467-083-42	Sequence 42, App1
21	24	55.8	15	1 US-08-414-417B-42	Sequence 42, App1
22	24	55.8	15	2 US-08-486-448A-42	Sequence 42, App1
23	24	55.8	15	2 US-08-468-545B-42	Sequence 42, App1
24	24	55.8	15	3 US-08-466-580B-42	Sequence 42, App1
25	24	55.8	17	1 US-08-237-118-24	Sequence 24, App1
26	24	55.8	19	3 US-08-486-099-141	Sequence 14, App1
27	24	55.8	19	3 US-08-484-223B-141	Sequence 14, App1
28	24	55.8	19	3 US-08-919-597-141	Sequence 14, App1

ALIGNMENTS

RESULT 1
US-08-467-083-27
; Sequence 27, Application US/08467083
; Patent No. 5726023
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.1, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467/083
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/414-417
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDBERRY
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: Linear
; US-08-467-083-27
; Query Match 100.0%; Score 43; DB 1; Length 9;
; Best Local Similarity 100.0%; Pred. No. 1.2e+05;
; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 K1FGSLAFL 9
11111111
Db 1 K1FGSLAFL 9

RESULT 2
US-08-787-547-70
; Sequence 70, Application US/08787547
; Patent No. 5785567

GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; CURLEY, Joanne M.
; APPLICANT: Langer, Robert S.
; TITLE OF INVENTION: MICROARTICLES FOR DELIVERY
; TITLE OF INVENTION: OF NUCLEIC ACID
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ FOR WINDOWS Version 2.0

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/787,547
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEX: 200154

INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-08-787-547-70

Query Match 100.0%; Score 43; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 0; Mismatches 0; Indels 0; Gaps 0;
; Gaps 0;

Qy 1 K1FGSLAFL 9
11111111
Db 1 K1FGSLAFL 9

RESULT 3
US-08-414-417B-27
; Sequence 27, Application US/0841417B
; Patent No. 5801005

GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; DISLER, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,417B
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-414-417B-27

Query Match 100.0%; Score 43; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 0; Mismatches 0; Indels 0; Gaps 0;
; Gaps 0;

Qy 1 K1FGSLAFL 9
11111111
Db 1 K1FGSLAFL 9

RESULT 4
US-08-486-348A-27
; Sequence 27, Application US/08486348A
; Patent No. 5846538

GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; DISLER, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,348A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900

```

; Sequence 18, Application US/08902516
; Patent No. 5891432
; GENERAL INFORMATION:
; APPLICANT: Soo Hoo, William
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLogy: linear
; US-08-486-348A-27

Query Match 100.0%; Score 43; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+05; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Del 0;
Db 1 KIFGSLAFL 9

RESULT 5
US-08-468-545B-27
; Sequence 27, Application US/08468545B
; Patent No. 5876712
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; ADDRESS: Seed and Berry LLP
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CURRENT APPLICATION DATA:
; TELEPHONE: (206) 622-6900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,545B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-6900
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLogy: linear
; US-08-468-545B-27

Query Match 100.0%; Score 43; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+05; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Del 0;
Db 1 KIFGSLAFL 9

RESULT 7
US-08-466-680B-27
; Sequence 27, Application US/08466680B
; Patent No. 6075122
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; ADDRESS: Seed and Berry LLP
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CURRENT APPLICATION DATA:
; TELEPHONE: (206) 622-6900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,680B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-6900
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLogy: linear
; US-08-468-545B-27

Query Match 100.0%; Score 43; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+05; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Del 0;
Db 1 KIFGSLAFL 9

RESULT 6
US-08-902-516-18

```

APPLICATION NUMBER: US/08/4666, 680B
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Sharkey, Richard G.
 REGISTRATION NUMBER: 32,629
 REFERENCE/DOCKET NUMBER: 9200010.448C4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-466-680B-27

Query Match 100.0%; Score 43; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 KIFGSLAFL 9
 Db 1 KIFGSLAFL 9

RESULT 8
 PCT-US5-16415-10
 Sequence 10, Application PC/"US9516415
 ; GENERAL INFORMATION:
 ; APPLICANT: The Scripps Research Institute
 ; TITLE OF INVENTION: IN VIVO ACTIVATION OF TUMOR-SPECIFIC
 ; CELLS
 ; NUMBER OF SEQUENCES: 38
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: The Scripps Research Institute
 ; STREET: 10666 North Torrey Pines Road, TPC-8
 ; CITY: La Jolla
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/16415
 FILING DATE: 13-DEC-1995
 CLASSIFICATION
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/3555, 5558
 FILING DATE: 14-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Logan, April C.
 REGISTRATION NUMBER: 33,950
 REFERENCE/DOCKET NUMBER: 433.1PC
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 554-2937
 TELEFAX: (619) 554-6312
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 PCT-US5-16415-10

Query Match 100.0%; Score 43; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 KIFGSLAFL 9
 Db 1 KIFGSLAFL 9

RESULT 9
 US-08-467-083-62
 Sequence 62, Application US/08467083
 ; Patent No. 5726023
 ; GENERAL INFORMATION:
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: Disis, Mary L.
 ; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
 ; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
 ; HER-2/neu ONCOGENE IS ASSOCIATED
 ; NUMBER OF SEQUENCES: 68
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Seed and Berry
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: US
 ; ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467, 083
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/414, 417
 FILING DATE: 06-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Sharkey, Richard G.
 REGISTRATION NUMBER: 32,629
 REFERENCE/DOCKET NUMBER: 920010.448C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-5031
 TELFEX: 3723836 SEEDANBERRY
 INFORMATION FOR SEQ ID NO: 62:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-467-083-62

Query Match 100.0%; Score 43; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.0e+00;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 KIFGSLAFL 9
 Db 1 KIFGSLAFL 9

RESULT 10
 US-08-414-417B-62
 Sequence 62, Application US/08414417B
 ; Patent No. 5801005
 ; GENERAL INFORMATION:
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: Disis, Mary L.
 ; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
 ; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
 ; HER-2/neu ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Seed and Berry LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: US
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/414,417B
 FILING DATE: 31-MAR-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Sharkey, Richard G.
 REGISTRATION NUMBER: 32,629
 REFERENCE/DOCKET NUMBER: 920010.448C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 62:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-414-417B-62

Query Match 100.0% Score 43; DB 2; Length 16;

Best Local Similarity 100.0% Pred. No. 0.0076; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9

Db 1 KIFGSLAFL 9

Query Match 100.0% Score 43; DB 2; Length 16;

Best Local Similarity 100.0% Pred. No. 0.0076; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9

Db 1 KIFGSLAFL 9

Query Match 100.0% Score 43; DB 2; Length 16;
 Best Local Similarity 100.0% Pred. No. 0.0076; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9

Db 1 KIFGSLAFL 9

Query Match 100.0% Score 43; DB 2; Length 16;
 Best Local Similarity 100.0% Pred. No. 0.0076; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9

Db 1 KIFGSLAFL 9

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 62:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-414-417B-62

RESULT 12
 Sequence 62, Application US/08468545B
 Patent No. 5876712
 GENERAL INFORMATION:
 APPLICANT: Cheever, Martin A.
 ATTORNEY/AGENT INFORMATION:
 DISIS, Mary L.
 TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
 TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu ONCOGENE IS ASSOCIATED
 NUMBER OF SEQUENCES: 69
 CURRENT APPLICATION ADDRESS:
 ADDRESSEE: Seed and Berry LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: US
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/468545B
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Sharkey, Richard G.
 REGISTRATION NUMBER: 32,629
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 62:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-414-417B-62

RESULT 11
 Sequence 62, Application US/08486348A
 Patent No. 5846538
 GENERAL INFORMATION:
 APPLICANT: Cheever, Martin A.
 ATTORNEY/AGENT INFORMATION:
 DISIS, Mary L.
 TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
 TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu ONCOGENE IS ASSOCIATED
 NUMBER OF SEQUENCES: 69
 CURRENT APPLICATION ADDRESS:
 ADDRESSEE: Seed and Berry LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: US
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/486,348A
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Sharkey, Richard G.
 REGISTRATION NUMBER: 32,629
 REFERENCE/DOCKET NUMBER: 920010.448C6

RESULT 13
 US-08-466-630B-62
 ; Sequence 62, Application US/08466680B
 ; GENERAL INFORMATION:
 ; APPLICANT: Cheever, Martin A.
 ; ADDRESS: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: US
 ; ZIP: 98104-7052
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 4.24
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sharkey, Richard G.
 ; REGISTRATION NUMBER: 32,629
 ; REFERENCE/DOCKET NUMBER: 920010.448C2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; TELEX: 3723836 SEEDBERRY
 ; INFORMATION FOR SEQ ID NO: 36:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; US-08-467-083-36

Query Match 67.4%; Score 29; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIFGSL 6
 Db 10 KIFGSL 15

RESULT 15
 US-08-414-417B-36
 ; Sequence 36, Application US/08414417B
 ; Patent No. 5801005
 ; GENERAL INFORMATION:
 ; APPLICANT: Cheever, Martin A.
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Disis, Mary L.
 ; REGISTRATION NUMBER: 32,629
 ; REFERENCE/DOCKET NUMBER: 920010.448C4
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 16 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; US-08-466-630B-62

Query Match 100.0%; Score 43; DB 3; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.0076;
 Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIFGSLAFL 9
 Db 1 KIFGSLAFL 9

RESULT 14
 US-08-467-083-36
 ; Sequence 36, Application US/08467083
 ; Patent No. 5726023
 ; GENERAL INFORMATION:
 ; APPLICANT: Cheever, Martin A.
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Disis, Mary L.
 ; REGISTRATION NUMBER: 32,629
 ; REFERENCE/DOCKET NUMBER: 920010.448C2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 36:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear

US-08-417B-36

Query Match 67.4%; Score 29; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIFGSL 6

Db 10 KIFGSL 15

RESULT 16

US-08-486-348A-36

; Sequence 36, Application US/08486348A

; GENERAL INFORMATION:

; APPLICANT: Cheever, Martin A.

; ATTORNEY/AGENT INFORMATION:

; NAME: Sharkey, Richard G.

; ADDRESS: Seed and Berry LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/486,348A

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 424

; NAME: Sharkey, Richard G.

; REGISTRATION NUMBER: 32,629

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 36:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; TOPOLOGY: Linear

; US-08-486-348A-36

; Query Match 67.4%; Score 29; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIFGSL 6

Db 10 KIFGSL 15

RESULT 17

US-08-468-545B-36

; Sequence 36, Application US/08468545B

; GENERAL INFORMATION:

; APPLICANT: Cheever, Martin A.

; ATTORNEY/AGENT INFORMATION:

; NAME: Sharkey, Richard G.

; ADDRESS: Seed and Berry LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/466,680B

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Sharkey, Richard G.

; REGISTRATION NUMBER: 32,629

; TELECOMMUNICATION INFORMATION:

; NUMBER OF SEQUENCES: 69

; CORRESPONDENCE ADDRESS:

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/468,548C4

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Sharkey, Richard G.

; REGISTRATION NUMBER: 920010.448C5

; TELECOMMUNICATION INFORMATION:

; NUMBER OF SEQUENCES: 69

; CORRESPONDENCE ADDRESS:

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; ZIP: 98104-7092

; NUMBER OF SEQUENCES: 69

; CORRESPONDENCE ADDRESS:

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/468,545B

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Sharkey, Richard G.

; REGISTRATION NUMBER: 32,629

; TELECOMMUNICATION INFORMATION:

; NUMBER OF SEQUENCES: 69

; CORRESPONDENCE ADDRESS:

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/468,545B

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Sharkey, Richard G.

; REGISTRATION NUMBER: 920010.448C5

; TELECOMMUNICATION INFORMATION:

; NUMBER OF SEQUENCES: 69

; CORRESPONDENCE ADDRESS:

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/468,545B

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Sharkey, Richard G.

; REGISTRATION NUMBER: 920010.448C5

; TELECOMMUNICATION INFORMATION:

; NUMBER OF SEQUENCES: 69

; CORRESPONDENCE ADDRESS:

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/468,545B

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Sharkey, Richard G.

; REGISTRATION NUMBER: 920010.448C4

; TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-466-660B-36

Query Match 67.48; Score 29; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KIFGSL 6
 Db 10 KIFGSL 15

RESULT 19
 US-08-215-805A-11
 Sequence 11; Application US/08215805A
 Patent No. 5553008

GENERAL INFORMATION:
 APPLICANT: Chang, Yung-Fu
 TITLE OF INVENTION: LEUKOTOXIN GENE FROM PASTURELLA
 TITLE OF INVENTION: suis
 NUMBER OF SEQUENCES: 84

CORRESPONDENCE ADDRESS:
 ADDRESSSEE: Nixon, Hargrave, Devans & Doyle
 STREET: Clinton Square, P.O. Box 1051
 CITY: Rochester
 STATE: New York
 COUNTRY: USA
 ZIP: 14603

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,083
 FILING DATE: 06-JUN-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/414,417
 FILING DATE: 0-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Sharkey, Richard G.
 REGISTRATION NUMBER: 32,629
 REFERENCE/DOCKET NUMBER: 920010-448C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 TELEX: 3723836 SEEDANBERRY
 INFORMATION FOR SEQ ID NO: 42:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-467-083-42

Query Match 55.8%; Score 24; DB 1; Length 15;
 Best Local Similarity 62.5%; Pred. No. 54;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KIFGSLAF 8
 Db 2 KVLGSGAF 9

RESULT 21
 US-08-414-417B-42
 Sequence 42; Application US/08414417B
 Patent No. 5801005

GENERAL INFORMATION:
 APPLICANT: Cheever, Martin A.
 TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: Seed and Berry LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: US
 ZIP: 98104 -7092

COMPUTER READABLE FORM:

Query Match 55.8%; Score 24; DB 1; Length 9;
 Best Local Similarity 83.3%; Pred. No. 1.2e+05;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 FGSLAF 8
 Db 2 FGSKAF 7

RESULT 20

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/414,417B
 FILING DATE: 31-MAR-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Sharkey, Richard G.
 REGISTRATION NUMBER: 32,629
 REFERENCE/DOCKET NUMBER: 920010.448C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 42:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-414-417B-42

Query Match 55.8%; Score 24; DB 2; Length 15;
 Best Local Similarity 62.5%; Pred. No. 54;
 Matches 5; Conservative 1; Mismatches 2; Indels 0;
 Gaps 0;

RESULT 23
 US-08-468-545B-42
 Sequence 42, Application US/08468545B
 ; Patent No. 5876712
 ; GENERAL INFORMATION:
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: Disis, Mary L.
 ; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
 ; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
 ; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
 ; NUMBER OF SEQUENCES: 69
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Seed and Berry LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: US
 ; ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/468-545B
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Sharkey, Richard G.
 REGISTRATION NUMBER: 32,629
 REFERENCE/DOCKET NUMBER: 920010.448C5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 42:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-468-545B-42

Query Match 55.8%; Score 24; DB 2; Length 15;
 Best Local Similarity 62.5%; Pred. No. 54;
 Matches 5; Conservative 1; Mismatches 2; Indels 0;
 Gaps 0;

RESULT 24
 US-08-466-680B-42
 Sequence 42, Application US/08466680B
 ; Patent No. 6075122
 ; GENERAL INFORMATION:
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: Disis, Mary L.
 ; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
 ; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
 ; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
 ; NUMBER OF SEQUENCES: 69
 ; CORRESPONDENCE ADDRESS:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/486-348A
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Sharkey, Richard G.
 REGISTRATION NUMBER: 32,629
 REFERENCE/DOCKET NUMBER: 920010.448C6
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 42:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-486-348A-42

ADDRESSEE: Sed and Berry LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: US
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/4666,680B
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Sharkey, Richard G.
 REGISTRATION NUMBER: 32,629
 REFERENCE/DOCKET NUMBER: 920010.448C4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 42:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-4666-680B-42

Query Match 55.8%; Score 24; DB 3; Length 15;
 Best Local Similarity 62.5%; Pred. No. 54;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 KIFGSLAF 8
 Db 1:111
 2 KVLGSGAF 9

RESULT 25
 US-08-237-418-24
 Sequence 24, Application US/08237418
 Patent No. 5601973
 GENERAL INFORMATION:
 APPLICANT: Mueller, Martin
 APPLICANT: Gissmann, Lutz
 TITLE OF INVENTION: Seroactive Regions on HPV 16 Proteins
 TITLE OF INVENTION: E1 and E2
 NUMBER OF SEQUENCES: 44
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &
 STREET: 1300 I Street, N.W., Suite 700
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-3315
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/237,418
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/913,613
 FILING DATE: 16-JUL-1992
 APPLICATION NUMBER: DE P 41 23 760.9
 FILING DATE: 18-JUL-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Einaudi, Carol P.

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2000, 11:56:53 : Search time 14.72 Seconds
(without alignments)
20.907 Million cell updates/sec

Title: US-09-277-074-10

Perfect score: 43 1 KIFGSLAFL 9

Sequence: Scoring table: BLOSUM62

Gapop 10.0 , Gapext. 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 127583

Post-processing: Minimum Match 0*

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_36:*

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2: /SIDS1/seqdata/geneseq/geneseq/AA1981.DAT:*

3: /SIDS1/seqdata/geneseq/geneseq/AA1983.DAT:*

4: /SIDS1/seqdata/geneseq/geneseq/AA1984.DAT:*

5: /SIDS1/seqdata/geneseq/geneseq/AA1985.DAT:*

6: /SIDS1/seqdata/geneseq/geneseq/AA1986.DAT:*

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21: /SIDS1/seqdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	9	15 R73685	Antigen fragment 1
2	43	100.0	9	17 R97507	Cytotoxic T lympho
3	43	100.0	9	18 W36824	Immunogenic peptide
4	43	100.0	9	19 W77131	HER 2/neu synthet
5	43	100.0	9	19 W78859	HER 1/neu protein
6	43	100.0	9	20 W70057	HER 2/neu derived
7	43	100.0	9	20 Y10495	HLA Class I motif
8	43	100.0	15	21 Y98846	HLA Class II bindi
9	29	67.4	17	21 Y86381	Human gene 16-enoo
10	25	58.1	7	20 Y48923	Membrane dipeptida
11	25	58.1	16	21 Y84219	Amino acid sequenc
12	58.1	16	21 Y84229	Amino acid sequenc	

RESULT 1

Antigen fragment 1, from c-ERB2 has binding affinity for HLA-2.1.

ID R73685 standard; peptide: 9 AA.

XX R73685;

XX DT 14-JUN-1995 (first entry)

DE XX

XX XX

Antigen fragment 1, from c-ERB2 has binding affinity for HLA-2.1.

ID R73685 standard; peptide: 9 AA.

XX R73685;

XX DT 14-JUN-1995 (first entry)

DE XX

XX XX

Antigen fragment 1

Cytotoxic T lympho

Immunogenic peptide

HER 2/neu synthet

HER 1/neu protein

HER 2/neu derived

HLA Class I motif

HLA Class II bindi

Human gene 16-enoo

Membrane dipeptida

Amino acid sequenc

Antigen fragment 1

Cytotoxic T lympho

Immunogenic peptide

HER 2/neu synthet

HER 1/neu protein

HER 2/neu derived

HLA Class I motif

HLA Class II bindi

Human gene 16-enoo

Membrane dipeptida

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Antigen fragment 1

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Immunogenic peptide

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HER 2/neu synthet

HER 1/neu protein

HER 2/neu derived

HLA Class I motif

HLA Class II bindi

Human gene 16-enoo

Membrane dipeptida

Amino acid sequenc

Antigen fragment 1

Cytotoxic T lympho

Immunogenic peptide

HER 2/neu synthet

HER 1/neu protein

HER 2/neu derived

HLA Class I motif

HLA Class II bindi

Human gene 16-enoo

Membrane dipeptida

Amino acid sequenc

Amino acid sequenc

Amino acid sequenc

A

X WPI: 1994-302678/37.
X Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
X for treatment or prophylaxis of cancer, virus infection or
X autoimmune diseases.
X Disclosure: Page 80; 138pp; English.
X S

similar compounds which may be useful for treating cancer or virally-infected cells, or for diagnosis. The peptide and vaccines produced provide immunity to a high percentage of different ethnic groups, i.e. those with different HLA alleles.

Disclosure: Page 80; 138pp; English.
R73685-876 are potential peptide binders of HLA-A2.1 motif. Using motifs disclosed in the invention, these peptides were screened for further motifs. Only peptides with binding affinity of at least 1 to the binding motif is expressed as an IC50 value) as compared to the standard peptide (R71293) in assays. This peptide has an binding value of 0.1500. The peptides of the invention can induce cytotoxic T lymphocytes which can react with target cells. They can be used for the treatment or prophylaxis of cancer, e.g. prostate cancer or lymphoma, etc.

Query	Match	Score	DB	Length	9;
Query 1	KIFGSLAFL 9	100.0%	43	9	
Best Local Matches	100.0%	100.0%	Pred. No.	2.1e+05;	
Matches	9;	Conservative	Mismatches	0;	Indels
				0;	Gaps

```

Query Match      100 0%;  Score 43;  DB 15;  Length 9;
Best Local Similarity 100.0%;  Pred. No. 2.1e+05;
Matches 9;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0

Y  1 KIFGSIAFL 9
   ||||| ||| 1 kifgsiafl 9

RESULT 2
97507 R97507 standard: peptide; 9 AA.
X
X
C R97507;
X
X
X 11-FEB-1997 (first entry)
X
X
X Cytotoxic T lymphocyte-activating Her-2/Neu-specific peptide.
X
X
X P53; Her-2; Neu; aa; amino acid; CTL; cytotoxic T lymphocyte; target;
X
X
X malignant cell; antigenic; vaccine; immunisation; activation.
X

```

AC	W36824;
XX	
DT	23-MAR-1998 (first entry)
XX	
DE	Immunogenic peptide H3 based on the human Her-2/neu protein.
XX	
KW	Her-2/neu protein; human leukocyte antigen A2.1; HLA;
KW	cytotoxic T lymphocyte; CTL; immune response; tumour associated antigen;
KW	T-cell receptor; TCR; tumour treatment.

97507	D	R97507 standard; peptide; 9 AA.
	X	
	C	R97507;
	X	
	X	11-FEB-1997 (first entry)
	X	
	E	Cytotoxic T lymphocyte-activating Her-2/Neu-specific peptide.
	W	P53; Her-2; Neu; aa; amino acid; CTL; cytotoxic T lymphocyte; target; malignant cell; antigenic; vaccine; immunisation; activation.
	W	
	X	Homo sapiens.
	S	

X 11-FEB-1997 (first entry)
 X Cytotoxic T lymphocyte-activating Her-2/Neu-specific peptide.
 X P53; Her-2; Neu; aa; amino acid; CTL; cytotoxic T lymphocyte; target;
 X malignant cell; antigenic; vaccine; immunisation; activation.
 X S Homo sapiens.

PPD 12-SEP-1997. PF 05-MAR-1997: 97W0-US03611.
XX

^A p53; Her-2; Neu; aa; amino acid; CTL; cytotoxic T lymphocyte; target; malignant cell; antigenic; vaccine; immunisation; activation.
^B Homo sapiens.

PR 05-MAR-1996: 9605-0012845.
XX (SCRI) SCRIPPS RES INST.
PA

W 3394902 R.L.
X X
20-JUN-1996.
X

DR XX Nucleic acid encoding variable regions of HLA-restricted non-human T cell receptor specific for tumour antigen - used to identify tumour
WT 199-74/0496/4-3.

R 14-DEC-1984 ; 94US-0355558.
 X (SCRI) SCRIPPS RES INST.
 X I Sherman LA;
 X WPI: 1996-30035/30.
 X In vivo activation of tumour-specific cytotoxic T lymphocytes - by
 X contacting with polypeptide(s) derived from human p53 or Her-2/Neu
 X proteins

PS Example 1: Page 9: 34pp; English.
XX Synthetic peptides W36824-40 are based on the sequence of the human
CC Her-2/neu protein, wherein each sequence contains the anchor motif for
CC human leukocyte antigen (HLA) A2.1. The present peptide is based on
CC positions 369-377. The ability of these peptides to inhibit the binding
CC of an influenza virus matrix protein M1 to HLA A2.1 was measured
CC by inhibition of lysis by a M1 specific HLA A2.1 restricted, cytotoxic
CC T-lymphocyte (CTL) clone. The present protein showed 38 inhibition. The
CC peptides were also tested for their ability to elicit an immune response
CC in vivo. However, only H3 (W36824) and H7 (W36826) were able to do
CC this. H3 and H7 peptides are tumour associated antigens and are
CC involved in the immune response to cancer.

R97507 is a peptide capable of activating cytotoxic T lymphocytes (CTLs) which specifically target malignant cells. The peptide corresponds to amino acids 369-377 of human Her-2/neu protein. CTL-activating peptides can be used in a vaccine for protecting against tumour cell formation. CTLs activated by the peptides will lyse tumour cells displaying specific peptides. Antibodies against CTL-activating peptides are useful for the identification of other tumour cells.

express at least one HLA antigen), so that the animal produces CTL which displays HLA-restricted T-cell receptor (TCR) specificity for the antigen. Nucleic acid encoding variable regions of the alpha and beta chains of such TCRs can be amplified from CTLs produced in the above manner. Cells expressing recombinant TCR are used to identify antigens associated with tumour and to treat tumours in humans. Transgenic mice are a more convenient source of CTL than the tumour infiltrating lymphocytes previously used. TCR can be humanised to reduce

CC side-reactions and short peptide derivatives of TCR are more economical
 CC to produce than TCR itself, particularly when expressed as a
 CC single-chain molecule rather than as a dimer.

SQ Sequence 9 AA;

Query Match 100.0%; Score 43; DB 18; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DE HER-1/neu protein fragment 369-377.
 KW Microparticle; delivery; polymeric matrix; autoantigen; tumour antigen;
 KW class II associated peptide; pathogen; gene therapy; genetic disease;
 KW infection; downregulation; immune response.
 XX
 OS Homo sapiens.
 OS synthetic.

RESULT 4

W77131 ID W77131 standard; peptide; 9 AA.
 XX
 AC W77131;
 XX
 DT 16-NOV-1998 (first entry)
 XX
 DE HER-2/neu synthetic peptide epitope 1.
 XX
 KW Tyrosinase; tyrosinase cytotoxic lymphocyte response;
 KW cytotoxic T lymphocyte; cysteine-depleted; melanoma.
 XX
 OS Synthetic.

PN W09833810-A2.

XX
 PD 06-AUG-1998.
 XX
 PF 29-JAN-1998; 98WO-US01592.
 XX
 PR 30-JAN-1997; 97US-0037781.
 XX
 PA (UVV1-) UNTV VIRGINIA PATENT FOUND.

PS Disclosure: Page 27: 93pp; English.

XX
 The peptide epitope W77119-W77138 were created for human tumour-specific
 CC cytotoxic T lymphocyte response. These peptides are are cysteine-
 CC depleted mutants of a native disease-specific CTL epitope. The cysteine-
 CC depleted CTL epitopes elicit a stronger or more specific CTL response
 CC than the native epitope. The epitopes can be used in a disease-specific
 CC immunogen to protect a mammal against disease in particular melanomas.
 CC The peptides may also be used to screen a sample for the presence of
 CC an antigen with the same epitope, or with a different cross-reactive
 CC epitope.

XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 43; DB 19; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DE HER-1/neu protein fragment 369-377.
 KW Microparticle; delivery; polymeric matrix; autoantigen; tumour antigen;
 KW class II associated peptide; pathogen; gene therapy; genetic disease;
 KW infection; downregulation; immune response.
 XX
 OS Homo sapiens.
 OS synthetic.

RESULT 6

Query Match 100.0%; Score 43; DB 19; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 K1FGSLAFL 9
 Db 1 k1fgslaf1 9
 RESULT 6
 W70057

ID	W70057	standard; peptide; 9 AA.	ID	Y10495	standard; Peptide; 9 AA.
XX	W70057;		XX	Y10495;	
AC			AC	Y10495;	
XX	22-OCT-1998	(first entry)	XX	12-MAY-1999	(first entry)
DT			DT		
XX	HER-2/neu derived HLA-A2.1 binding peptide 5 (residues 369-377).		XX	HLA Class I motif peptide SEQ ID NO:425.	
DIE			DE		
XX	Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;		XX	Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;	
KW	human leukocyte antigen; HLA; tumour associated antigen; cancer;		KW	immunisation; tumour; infectious disease; immunotherapy; cancer;	
KW	antigen presenting cell; APC; immunogenic peptide; immune disorder;		KW	malignant melanoma; viral disease; hepatitis; AIDS.	
KW	viral infection; AIDS; hepatitis; bacterial infection; malaria;		XX		
KW	fungal infection; tuberculosis; melanoma; HER-2/neu; cerB-2.		OS	Synthetic.	
OS			OS	Homo sapiens.	
XX	Synthetic.		XX		
OS	Itino sapiens.		PN	WO902183-A2.	
XX			XX		
PN	WO9333888-A1.		PD	21-JAN-1999.	
XX			XX		
PD	06-AUG-1998.		PF	10-JUL-1998;	98WO-US14289.
XX			XX		
PF	30-JAN-1998;	98WO-US01959.	PR	10-DEC-1997;	97US-0988320.
XX			PR	10-JUL-1997;	97CA-2209815.
PR	31-JAN-1997;	97US-0036696.	XX		
XX			PA	(CTLI-) CTL IMMUNOTHERAPIES CORP.	
PA	(EPIM-) EPIMMUNE INC.		XX		
XX			PI	Kuendig TM, Simard JJL;	
PI	Cellis E, Sette A, Sidney J, Southwood S, Tsai V;		XX		
XX			DR	WPI; 1999-120514/10.	
DR	1998-437445/37.		XX		
XX			PT	Inducing a cytotoxic T lymphocyte response - by maintaining a level	
PT	Production of antigen-specific cytotoxic T cells - by incubating		PT	of antigen in the lymphatic system of a mammal so as to provide a	
PT	immunogenic peptide(s) from antigen that binds class I major		PT	sustained CTL response, used to treat, e.g. AIDS	
PT	histocompatibility complex molecules with pre-treated antigen		XX		
PT	presenting cells		PS	Disclosure; Page 43; 199pp; English.	
XX			XX		
PS	Example 7; Page 77; 104pp; English.		CC	The present invention describes a method of inducing and/or sustaining	
XX			CC	an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The	
CC	method comprises: (a) delivering an antigen to the mammal at a level to		CC	induce an immunological CTL response in the mammal; and (b) maintaining	
CC	the level of the antigen in the mammal's lymphatic system to maintain		CC	the immunological CTL response. The method can be used for the delivery of	
CC	the immunological CTL response, e.g. a differentiation antigen, a tumour-specific multilineage antigen,		CC	e.g. an embryonic antigen, an oncogene antigen, a mutated tumour-suppressor	
CC	gene antigen, or a viral antigen. They can be used for the treatment of		CC	gene antigen, or a viral antigen. They can be used for the treatment of	
CC	CC disease such as cancer, e.g. malignant melanoma or infectious disease,		CC	CC e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery	
CC	CC to the lymphatic system provides for potent CTL stimulation that takes		CC	CC place in the milieu of the lymphoid organ, and it sustains stimulation	
CC	CC that is necessary to keep CTL active, cytotoxic and recirculating		CC	CC through the body. Y10071 to Y10639 represent examples of peptide	
CC	CC antigens given in the present invention.		CC	CC	
XX			XX	Sequence 9 AA;	
XX			Query	1. KIFGSLAFL 9	
XX			Match		
XX			Best Local Similarity	100.0%	Score 43; DB 20; Length 9;
XX			Matches	9; Conservative 0;	Pred. No. 2.1e+05; Mismatches 0; Indels 0; Gaps 0;
Qy	1 KIFGSLAFL 9		RESULT	8	
DB			ID	Y98846	
DB	1 kifgsiaf 9		AC	Y98846	
DB			XX		
RESULT	7		DT	07-AUG-2000 (first entry)	
Y10495			XX		

DE HLA class II binding antigen epitope peptide #35.
 XX Y86381;
 KW Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical;
 KW immune response; chronic viral disease; cancer; autoimmune disease;
 KW rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS;
 KW allograft rejection; allergy; lyme disease; hepatitis; prostate cancer;
 KW glomerulonephritis; food hypersensitivity; malaria.
 XX Unidentified.
 XX WO961916-A1.
 XX PD 02-DEC-1999.
 XX PF 28-MAY-1999; 99WO-US12066.
 XX PR 29-MAY-1998; 98US-0087192.
 XX PA (EPIIM-) EPIMMUNE INC.
 PI Sette A, Southwood S, Sidney J;
 XX DR WPI: 2000-097143/08.
 XX PT New compositions containing immunogenic peptide epitopes for various
 HLA class II DR molecules useful for inducing helper T cell response -
 XX PS Claim 1; Page 40; 60pp; English.
 CC The present invention relates to a new pharmaceutical composition
 comprising a unit dose form of a peptide, or analogue, comprising an
 epitope selected from those represented by peptides Y9812-Y9939 which
 are derived from various antigens for various human leucocyte antigen
 class DR molecules, representative of the world wide population. The
 peptide/analogue binds to an HLA class II molecule at an IC-50 of less
 than or equal to 1,000 nM. The pharmaceutical can be used to induce a
 helper T cell response. The pharmaceutical focuses the immune response
 towards selected determinants and could therefore be used in cases of
 chronic viral diseases and cancer. Examples of diseases that can be
 treated using the peptide containing pharmaceutical include autoimmune
 diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia
 gravis), alloraft rejection, allergies, lyme disease, hepatitis,
 post-streptococcal endocarditis or glomerulonephritis, and food
 hypersensitivities. The peptide epitopes can be used to enhance immune
 responses against other immunogens administered with the peptides.
 CC Diseases which can be treated using immunogenic mixtures include prostate
 cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical
 carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be
 used to make monoclonal antibodies useful as potential diagnostic or
 therapeutic agents. The peptides may also be useful as diagnostic
 reagents, for example, to determine the susceptibility of an individual
 to a treatment regimen. Also, the peptides may be used to predict which
 individuals will be at substantial risk of developing chronic infection.
 CC The selection of appropriate T and B cell epitopes should allow the
 development of epitope based vaccines particularly towards conserved
 epitopes of pathogens which are characterized by high sequence
 variability such as HIV, HCV and Malaria.
 XX Sequence 15 AA;
 SQ Score 43; DB 21; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.009; Mismatches 0; Indels 0; Gaps 0;

DE Human gene 16 encoded protein fragment, SEQ ID NO:296.
 XX Human gene 16 encoded protein fragment, SEQ ID NO:296.
 DE Human gene 16 encoded protein fragment, SEQ ID NO:296.
 KW Human; secreted protein; cancer; tumour; developmental abnormality;
 KW foetal deficiency; blood disorder; immune system disorder; inflammation;
 KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
 KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
 KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
 KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
 KW therapy.
 XX OS Homo sapiens.
 XX PN WO966041-A1.
 XX PD 23-DEC-1999.
 XX PP 15-JUN-1999; 99WO-US13418.
 XX PR 16-JUN-1998; 98US-0089507.
 XX PR 16-JUN-1998; 98US-0089508.
 XX PR 16-JUN-1998; 98US-0089509.
 XX PR 16-JUN-1998; 98US-0089510.
 XX PR 22-JUN-1998; 98US-0090112.
 XX PR 22-JUN-1998; 98US-0090113.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Ruben SM, Ni J, Rosen CA, Wei Y, Young PE, Florence KA;
 PI Sopko DR, Brewer LA, Endress GA, Carter KC, Mucinski M, Ebner R;
 PI Lafleur DW, Olsen HS, Shi Y, Moore PA, Komatsoulis G;
 XX DR WPI; 2000-106100/09.
 XX New isolated human genes and the secreted polypeptides they encode,
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders -
 XX Disclosure; Page 34; 586pp; English.
 XX Z97019 to Z97137 represent 94 isolated human secreted protein genes.
 CC Y86215 to Y86332 are the secreted proteins encoded by the 94 human genes.
 CC This sequence represents a fragment of one of the human secreted
 CC proteins. The genes and their corresponding secreted polypeptides are
 CC useful for preventing, treating or ameliorating medical conditions, e.g.,
 CC by protein or gene therapy. Also pathological conditions can be
 CC diagnosed by determining the amount of the new polypeptides in a sample
 CC or by determining the presence of mutations in the new genes. Specific
 CC uses are described for each of the 94 genes, based on which tissues they
 CC are most highly expressed in, and include developing products for the
 CC diagnosis or treatment of cancer, tumours, developmental abnormalities
 CC and foetal deficiencies, blood disorders, diseases of the immune system,
 CC autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive
 CC disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin
 CC disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney
 CC disorders, digestive/endocrine disorders, infections and AIDS. The
 CC polypeptides are also useful for identifying their binding partners.
 CC The sequences shown in Y86334 to Y86585 represent fragments of the
 CC secreted proteins.
 XX Sequence 17 AA;
 SQ Score 29; DB 21; Length 17;
 Best Local Similarity 50.0%; Pred. No. 8.3; Mismatches 4; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
 DB 3 kifgslaf 11

RESULT 9
 Y86381 standard; peptide: 17 AA.

Query Match 67.4%; Score 29; DB 21; Length 17;
 Best Local Similarity 50.0%; Pred. No. 8.3; Mismatches 4; Indels 0; Gaps 0;
 Matches 4; Conservative 2 IFGSLAFL 9
 :||:|||

Db	2	vygsmstf1	9
RESULT	10		
Y48923	ID	Y48923 standard; Peptide; 7 AA.	
XX	XX		
Y48923;	AC		
XX	AC		
10-DEC-1999	DT	(first entry)	
XX	XX		
Membrane dipeptidase-binding ovary homing peptide #11.	DE		
XX	XX		
Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP; prostate; ovary; lymph node; adrenal gland; liver; gut; tumour; membrane dipeptidase.	KW		
XX	XX		
Synthetic.	OS		
Homo sapiens.	OS		
W09946284-A2.	PN		
XX	XX		
PD 16-SEP-1999.	PD		
XX	XX		
PF 10-MAR-1999; 99WO-US05284.	PF		
XX	XX		
PR 13-MAR-1998; 98US-0042107.	PR		
PR 26-FEB-1999; 99US-0042107.	PR		
XX	XX		
PA (BURN-) BURNHAM INST.	PA		
XX	XX		
Rajotte D, Pasqualini R, Ruoslahti EI;	PI		
XX	XX		
WPI: 1999-571717/48.	DR		
XX	XX		
New peptides which selectively home to organs or tissues, used for, e.g. identifying target ligands and for therapy of pathological conditions.	PT		
PT	PT		
Example 6; Page 152; 193pp; English.	PS		
XX	XX		
The present invention describes peptides that selectively home to a tissue or organ. The peptides can be used for identifying an organ or tissue, for identifying a target molecule expressed by an organ or tissue or for treating an organ or tissue pathology, where the organ or tissue is selected from prostate, lung, skin, retina, pancreas, gut, ovary, adrenal gland, liver, and lymph node. The peptide bind to the membrane dipeptidase (MDP). Y48618 to Y49066 represent sequences which are used in the exemplification of the present invention.	CC		
XX	CC		
Sequence 7 AA.	SQ		
Query Match 3 EGSTIAFL 9	QY		
Best Local Similarity 71.4%; Score 25; DB 20; Length 7;	QY		
Matches 5; Conservative 1; Indels 0; Gaps 0;	QY		
XX	XX		
Y84219	AC		
XX	AC		
03-JUL-2000 (first entry)	DT		
XX	XX		
Amino acid sequence of a peptide.	DE		
XX	XX		
RESULT 11	RESULT	11	
Y84219	ID	Y84219 standard; peptide; 16 AA.	
XX	XX		
Y84219;	AC		
XX	AC		
Y84229 standard; peptide; 16 AA.	ID	Y84229	RESULT 12
XX	XX		
Amino acid sequence of a peptide.	AC	Y84229;	
XX	XX		

XX Amino acid sequence of a peptide derived from site-1 protease.
 DE XX Antimicrobial peptide fragment from ubiquicidine (residues 1-18).
 DE XX Ubiquicidine; treatment; diagnosis; prophylaxis; infection; microbial;
 DE KW Pathogenic; Gram-positive bacteria; antimicrobial; Staphylococcus aureus;
 DE KW Klebsiella pneumoniae; Gram-negative; Klebsiella pneumoniae; E. coli;
 DE KW Enterococcus; Salmonella typhimurium; Mycobacterium avium; M. fortuitum;
 DE KW fungus; Candida albicans; Cryptococcus neoformans; Aspergillus fumigatus;
 DE KW virus; parasite; Trypanosoma cruzi; Taxoplasma gondii.
 DE XX Synthetic.
 OS OS Synthetic.
 OS OS Mus sp.
 XX XX WO9854314-A1.
 PN PN
 PD PD 03-DEC-1998.
 XX XX 99WO-US15544.
 PF PF 13-AUG-1999; 99WO-US15544.
 XX XX 29-MAY-1998; 98WO-NL00311.
 PR PR 14-AUG-1998; 98US-0096571.
 PR PR 23-JUL-1999; 99US-0360237.
 XX XX 29-MAY-1997; 97NL-1006164.
 PA PA (UYLE-) RIJKSUNIV LEIDEN.
 PA PA (TEXA) UNIV TEXAS SYSTEM.
 PA PA (BROW) BROWN M S.
 PA PA (CHEN) CHENG D.
 PA PA (ESPE) ESPENSHADE P J.
 PA PA (GOLD) GOLDSTEIN J L.
 PA PA (RANS) RAWSON R B.
 PA PA (SAKA) SAKAI J.
 PI PI Brown MS, Cheng D, Espenshade PJ, Goldstein JL, Rawson RB;
 PI PI Sakai J;
 XX XX DR; 2000-224327/19.
 XX XX Novel assay for identifying modulators of sterol-regulated Site-1 protease useful for the treatment of hypercholesterolemia, involves identifying an agent capable of down regulating Site-1 protease activity.
 XX Disclosure: Fig 24A; 172pp; English.
 XX The specification describes a method for identifying modulators of a sterol-regulated Site-1 protease. Site-1 protease cleaves sterol regulatory element binding proteins (SRBPs) in the endoplasmic reticulum, initiating release from membranes and activating lipid synthesis. The modulators therefore also modulate cholesterol and fatty acid biosynthesis. The method comprises selecting an agent capable of down regulating Site-1 protease and formulating a composition comprising the agent. The site-1 protease inhibitors are useful for treating a patient for elevated serum cholesterol. Diseases treated include hypercholesterolemia and other lipid metabolism associated conditions. The present sequence is derived from site-1 protease, and is used in the course of the invention.
 XX Sequence 16 AA;
 SQ Query Match 1 KIFGSLA 7
 Best Local Similarity |: | | |
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 RESULT 14
 W60420 DT 24-AUG-1998 (first entry)
 ID XX Tumour homing peptide of the invention.
 DE XX
 XX KW Tumour homing peptide; in vivo painting; murine melanoma; tumour.
 AC OS Synthetic.
 XX OS
 DR XX WO9810795-A2.
 PN PN

XX	19-MAR-1998.	Identifying molecules that home to angiogenic vasculature used as targets for anticancer agents
10-SEP-1997;	97WO-US16086.	
10-SEP-1996;	96US-0710067.	
(BURN-)	BURNHAM INST.	
Pasqualini, R.	Ruoslahti, E;	
WPI;	1998-207151/48.	
Tumour homing molecules and their conjugates - useful for, e.g., directing linked moiety to tumour containing angiogenic vasculature		
Example 5; Page 80; 105pp; English.		
w60390-032 represent peptides recovered from mouse melanomas. The peptides are tumour homing peptides, and are identified by in vivo panning. The in vivo panning comprises administering a library of diverse peptides to a subject having a tumour, collecting a sample of the tumour, identifying a peptide that homes to the tumour, collecting a sample of normal tissue corresponding to the tumour, and determining that the peptide that homes to the tumour is not present in the normal tissue. The tumour homing peptides can be linked to a moiety (e.g. doxorubicin), and used to direct the moiety to a tumour.		
Sequence 7 AA;		
Query Match 55.8%; Score 24; DB 19; Length 7; Best Local Similarity 83.3%; Pred. No 2.1e+05; Matches 0; Mismatches 1; Indels 0; Gaps 0;		
Qy 4 GSIAFL 9 Db 1 gsfaf1 6		
RESULT 15		
W93747		
W93747 standard; Peptide: 7 AA.		
W93747;		
28-JUN-1999 (first entry)		
Mouse B16B15b melanoma derived tumour homing peptide 32.		
Tumour homing peptide; tumour; diagnosis; endothelial cell; melanoma; angiogenic vasculature; anti-tumour; anti-inflammatory; anti-angiogenic; anti-arthritis; NGR receptor; inhibitor; angiogenesis; anticancer drug; prognosis; inflammation; regeneration; wounded tissue; targeting; macular degeneration; diabetic retinopathy; rheumatoid arthritis; occlusive thrombus; murine.		
Mus sp.		
W09913329-A1.		
18-MAR-1999.		
08-SEP-1998;	98WO-US18895	
25-AUG-1998;	98WO-0139802.	
10-SEP-1997;	97US-0926914.	
(BURN-)	BURNHAM INST.	
Pasqualini, R.	Ruoslahti, E;	
WPI;	1998-215159/48.	

XX WPI; 1999-122216/11.
 XX
 PT derivatives of calcitonin-gene-related peptide fragment - useful as
 PT diagnostic reagents and as CGRP antagonists, for treatment of
 PR cardiovascular diseases, headaches and asthma
 XX
 PS Claim 4; Page 18; 19pp; German.

The invention describes peptides derived from calcitonin-gene-related peptide (rCGRP-alpha) (positions 27-37) sequence H-FVPTNWSEAF NH2 where (i) 1-3 of the amino acids in the sequence FVPTNWSE are replaced with K, Y, A, F, P, Hyp, S, L, Q, D, H, Acp, Pac, Tic, Hop, Aib, I or G; or (ii) the sequence FVPTNWSE is replaced with NFVPRSKISP, NVAPRNSKSP, NVAPRNNGS or ILSNWGS; and/or (iii) 1-8 of the amino acids in the sequence FVPTNWSEAF are deleted and (iv) one amino acid in the sequence FVPTNWSEAF can be a D-amino acid and (v) the N-terminal amino group can be substituted by a protecting group R selected from 3,3-diphenylpropionyl, 2-propylpentanoyl, 3,5-dichlorophenoxyacetyl, 1-adamantyl acetyl, 3,5-dibromo-4-hydroxyphenylalanyl, 4-(4-benzydryl-1-piperazineyl)-1,5-dioxo-3,3-(tetramethylene)-pentyl or 1,5-dihydro-6-oxo-6H-dibenzo[b,e]azepin-11-carbonyl. The peptides are useful for treating headache, non-insulin-dependent diabetes mellitus, cardiovascular diseases, skin diseases, inflammatory diseases, allergic rhinitis, asthma, diseases involving excessive vascular dilation and concomitant reduced tissue blood flow, and morphine tolerance. They are also useful for producing and purifying antibodies, as immunoassay reagents, as diagnostic and analytical tools in neurotransmitter research.

XX Sequence 11 AA;
 XX
 Query Match 55.8%; Score 24; DB 20; Length 11;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GSQLAF 8
 Y98857 standard; Peptide: 15 AA.
 ID Y98857.
 AC Y98857;
 DT 07-AUG-2000 (first entry)

RESULT 17
 DE HLA class II binding antigen epitope peptide #46.

XX Human leucocyte antigen: HLA class II; antigen epitope: pharmaceutical; immune response; chronic viral disease; cancer; autoimmune disease; rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS; allograft rejection; allergy; lyme disease; hepatitis; prostate cancer; glomerulonephritis; food hypersensitivity; malaria.
 XX Unidentified.
 PN W09961916-A1.
 PD 02-DEC-1999.

XX
 PF 28-MAY-1999; 99WO-US12066.
 XX
 PR 29-MAY-1998; 98US-0087192.
 XX
 PA (EPIIM) - EPIMUNE, INC.
 XI Sette, A., Southwood, S., Sidney, J;
 XX
 DR WPI; 2000-097143/08.

XX New compositions containing immunogenic peptide epitopes for various DR HLA class II DR molecules useful for inducing helper T cell response
 PT
 PR
 PS Claim 1; Page 40; 60pp; English.
 XX
 CC The present invention relates to a new pharmaceutical composition comprising a unit dose form of a peptide, or analogue, comprising an epitope selected from those represented by peptides Y9812-Y9939 which are derived from various antigens for various human leucocyte antigen class DR molecules, representative of the world wide population. The peptide/analogue binds to an HLA class II molecule at an IC-50 of less than or equal to 1,000 nM. The pharmaceutical can be used to induce a helper T cell response. The pharmaceutical focuses the immune response towards selected determinants and could therefore be used in cases of chronic viral diseases and cancer. Examples of diseases that can be treated using the peptide containing pharmaceutical include autoimmune diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia gravis), allograft rejection, allergies, lyme disease, hepatitis, CCP post-streptococcal endocarditis or glomerulonephritis and food hypersensitivities. The peptide epitopes can be used to enhance immune responses against other immunogens administered with the peptides. Diseases which can be treated using immunogenic mixtures include prostate cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be used to make monoclonal antibodies useful as potential diagnostic or therapeutic agents. The peptides may also be useful as diagnostic reagents, for example, to determine the susceptibility of an individual to a treatment regimen. Also, the peptides may be used to predict which individuals will be at substantial risk of developing chronic infection. The selection of appropriate T and B cell epitopes should allow the development of epitope based vaccines particularly towards conserved epitopes of pathogens which are characterized by high sequence variability such as HIV, HCV and Malaria.

XX
 SQ Sequence 15 AA;

Query Match 55.8%; Score 24; DB 21; Length 15;
 Best Local Similarity 62.5%; Pred. No. 80;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KIFGSLAF 8
 Db 8 kvlgsgaf 15

RESULT 18
 ID R64603 standard; Peptide: 16 AA.
 XX
 AC R64603;
 DT 01-SEP-1995 (first entry)
 DE RF-1 peptide 48 from respiratory syncitial virus.
 XX antiviral activity: DP-178; DP-107; diagnostic: HIV-1/LAI;
 KW human immunodeficiency virus; transmembrane protein; gp41;
 KW alpha helix; leucine zipper; DP-185; respiratory syncitial virus;
 XX RSV.
 OS Synthetic.
 XX
 Key Location/Qualifiers
 FF Modified-site 1
 PR /note= "optionally has an amino, acetyl,
 FT 9-fluorenylmethoxy-carbonyl, hydrophobic or
 FT macromolecular carrier gp. attached."
 FT
 FT
 FT
 FT
 FT
 FT
 FT
 XX
 DR

PN WO9428920-A.
 XX PD 22-DEC-1994.
 XX PR 07-JUN-1994; 94WO-US05739.
 XX PR 07-JUN-1993; 93US-0073028.
 XX PA (UYDU-) UNIV DUKE.
 XX PR Computer search generated synthetic peptides - are inhibitors of HIV transmission
 XX PI Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;
 PI Petteway SR, Wild CT;
 XX DR WPI: 1995-036105/05.
 XX PT Computer search generated synthetic peptides - are inhibitors of HIV transmission
 XX PR Claim 14: Page 138; 182pp; English.
 XX PS Claim 14: Page 138; 182pp; English.
 CC R64591-623 are peptide derivatives of a 37 mer RF-1 peptide derived from respiratory syncytial virus (RSV) (R64590) which have been truncated at the amino terminus. The peptides are DP-178 like peptides. DP-178 corresponds to amino acids 638 to 673 of the HIV-1 isolate LAI transmembrane protein gp41. It forms a putative alpha helix at the C-terminal end of the gp41 ectodomain, and complexes with DP-107 (corresponds to amino acids 558-595) which contains a leucine zipper motif. The peptides complex via non-covalent protein-protein interactions. The peptide derivatives were identified by a computer assisted peptide sequence search. The antiviral activity of this peptide is not stated in the specification.
 CC Sequence 16 AA;
 XX SQ Query Match 55.8%; Score 24; DB 16; Length 16;
 Best Local Similarity 66.7%; Pred. No. 85; Indels 0; Gaps 0;
 Matches 6; Conservative 1; Mismatches 2;
 DE Qy 1 KIFGSSL AFL 9
 DE Db 1 kingslaf 9
 RESULT 20
 DE P30110
 DE ID P30110 standard; Protein; 18 AA.
 DE XX DT 03-APR-1992 (first entry)
 DE XX DE Sequence of VP1 capsid protein residues 141-160 from the amino terminus, FMDV, Tübingen type 0, subtype 1, strain Kaufbeuren.
 DE XX KW Antigen; Picornavirus; capsid protein; antibody; detection;
 DE XX KW vaccine; diagnosis.
 DE XX OS Foot and mouth disease virus.
 DE XX PN WO8303547-A.
 DE XX PD 27-OCT-1983.
 DE XX PR 14-APR-1983;
 DE XX PR 14-APR-1983;
 DE XX PR 14-APR-1983;
 DE XX PR 25-MAR-1983; 83US-0478847.
 DE XX PR 14-APR-1982; 82US-0366308.
 DE XX PR 20-SEP-1984; 84US-0653475.
 DE XX PR 18-DEC-1984; 84US-0682819.
 DE XX PA (BIRL/) BIRLE J L.
 DE PA (SCRIP-) SCRIPPS CLINIC & RE.
 DE XX PN WO9428920-A.

PI Bittle JL, Lerner RA;
 XW WPI: 1983-807942/44.
 DR Antigenic peptide(s) corresp. to picornavirus capsid protein -
 useful in prodn. of vaccines and in diagnostic tests
 PT Disclosure; Page 14; 90PP; English.
 XX

The peptides of the invention corresp. to a region on the antigenic
 picornavirus capsid protein. The capsid protein FMDV VP1 or Polio
 virus VP1. When linked to carriers the peptides are immunogenic.
 Dose is 20 ug-2mg peptide for inoculations.

XX Sequence 18 AA;

Query Match 55.8%; Score 24; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FGSLA 7
 |||||
 Db 7 fgsla 11

RESULT 21
 R64605 ID R64605 standard; Peptide; 18 AA.
 XX
 AC R64605;
 XX
 DT 01-SEP-1995 (first entry)
 XX RF-1 peptide 50 from respiratory syncitial virus.
 DE antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI;
 XX human immunodeficiency virus; transmembrane protein; gp41;
 KW alpha helix; leucine zipper; DP-185; respiratory syncitial virus;
 KW RSV.
 XX
 OS Synthetic.
 XX
 FH Key
 FT Modified-site 1 Location/Qualifiers
 FT /note= "optionally has an amino, acetyl,
 FT 9-fluorenylmethoxy-carbonyl, hydrophobic or
 FT macromolecular carrier gp. attached"
 FT Modified-site 18
 FT /note= "optionally has a carboxyl, amido, hydrophobic
 FT or macromolecular carrier gp. attached"
 XX WO9428920-A.
 PN 22-DEC-1994.
 PD 07-JUN-1994;
 XX 94W0-US05739.
 PR 07-JUN-1993;
 XX 93US-0073028.
 PA (UYDU-) UNIV DUKE.
 XX
 PI Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;
 PI Petteway SR, Wild CR;
 XX DR WPI: 1995-036105/05.
 XX
 PT Computer search generated synthetic peptides - are inhibitors of
 PT HIV transmission
 XX
 PS Claim 14; Page 138; 182PP; English.
 XX
 CC R64591-623 are peptide derivatives of a 37 mer RF-1 peptide derived
 CC from respiratory syncitial virus (RSV) (R64590) which have been
 CC truncated at the amino terminus. The peptides are DP-178 like

CC from respiratory syncitial virus (RSV) (R64590) which have been
 CC truncated at the amino terminus. The peptides are DP-178 like
 CC peptides. DP-178 corresponds to amino acids 638 to 673 of the HIV-1
 CC isolate LAI transmembrane protein gp41. It forms a putative alpha
 CC helix at the C-terminal end of the gp41 ectodomain, and complexes
 CC with DP-107 (corresponds to amino acids 558-595) which contains a
 CC leucine zipper motif. The peptides complex via non-covalent
 CC protein-protein interactions. The peptide derivatives were
 CC identified by a computer assisted peptide sequence search. The
 CC antiviral activity of this peptide is not stated in the
 CC specification.
 XX Sequence 18 AA;

Query Match 55.8%; Score 24; DB 16; Length 18;
 Best Local Similarity 66.7%; Pred. No. 96;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KIFGSLAFL 9
 ||| |||||
 Db 3 kingslaf 11

RESULT 22
 R64606 ID R64606 standard; Peptide; 19 AA.
 XX
 AC R64606;
 XX
 DT 01-SEP-1995 (first entry)
 XX RF-1 peptide 51 from respiratory syncitial virus.
 DE antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI;
 XX human immunodeficiency virus; transmembrane protein; gp41;
 KW alpha helix; leucine zipper; DP-105; respiratory syncitial virus;
 KW RSV.
 XX
 OS Synthetic.
 XX
 FH Key
 FT Modified-site 1 Location/Qualifiers
 FT /note= "optionally has an amino, acetyl,
 FT 9-fluorenylmethoxy-carbonyl, hydrophobic or
 FT macromolecular carrier gp. attached"
 FT Modified-site 19
 FT /note= "optionally has a carboxyl, amido, hydrophobic
 FT or macromolecular carrier gp. attached"
 XX WO9428920-A.
 PN 22-DEC-1994.
 PD 07-JUN-1994;
 XX 94W0-US05739.
 PR 07-JUN-1993;
 XX 93US-0073028.
 PA (UYDU-) UNIV DUKE.
 XX
 PI Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;
 PI Petteway SR, Wild CR;
 XX DR WPI: 1995-036105/05.
 XX
 PT Computer search generated synthetic peptides - are inhibitors of
 PT HIV transmission
 XX
 PS Claim 14; Page 138; 182PP; English.
 XX
 CC R64591-623 are peptide derivatives of a 37 mer RF-1 peptide derived
 CC from respiratory syncitial virus (RSV) (R64590) which have been
 CC truncated at the amino terminus. The peptides are DP-178 like

peptides. DP-178 corresponds to amino acids 638 to 673 of the HIV-1 isolate LAI transmembrane protein gp41. It forms a putative alpha helix at the C-terminal end of the gp41 ectodomain, and complexes with DP-107 (corresponds to amino acids 558-595) which contains a leucine zipper motif. The peptides complex via non-covalent protein-protein interactions. The peptide derivatives were identified by a computer assisted peptide sequence search. The specificity of this peptide is not stated in the specification.

peptides. DP-178 corresponds to amino acids 638 to 673 of the HIV-1 isolate LAI transmembrane protein gp41. It forms a putative alpha helix at the C-terminal end of the gp41 ectodomain, and complexes with DP-107 (corresponds to amino acids 558-595) which contains a leucine zipper motif. The peptides complex via non-covalent protein-protein interactions. The peptide derivatives were identified by a computer assisted peptide sequence search. The antiviral activity of this peptide is not stated in the specification.

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Query Match      55.8%;  Score 24;  DB 16;  Length 19;
Best Local Similarity 66.7%;  Pred. No. 1e+02;  0;
Matches          6;  Conservative 1;  Mismatches 2;  Indels 0;  Ga
y 1 KIFGSLAFL 9
y 4 kingslaFL 12

```

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Query Match      55.8%;  Score 24;  DB 16;  Length 19;
Best Local Similarity 66.7%;  Pred. No. 1e+02;
Matches 6;  Conservative 1;  Mismatches 2;  Indels 0;  Gaps 0;
                                         RESULT 24 *
                                         ID R64607 standard; Peptide: 20 AA
                                         XX
                                         AC R64607;
                                         XX
                                         DT 01-SEP-1995 (first entry)
                                         XX
Y 1 KIFGCSLAFL 9
| | | | | |;
O 4 kingslafl 12

```

RESULT	23	DE	RF-1 peptide 52 from respiratory syncitial virus.
39178	XX	XX	39178 standard; peptide; 19 AA.
Y89178	XX	KW	antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI;
X	X	KW	human immunodeficiency virus; transmembrane protein; gp41;
X	X	KW	alpha helix; leucine zipper; DP-185; respiratory syncitial virus;
X	X	KW	RSV.
X	X	KW	
23-MAY-2000	(first entry)	XX	
Core polypeptide fragment T No. 617.		OS	
X	X	Synthetic.	
X	X	XX	
X	X	Key	Location/Qualifiers
X	X	Modified-site	1
X	X	FH	
X	X	FT	
X	X	FT	/note= "optionally has an amino, acetyl,
X	X	FT	9-fluorenylmethoxy carbonyl, hydrophobic or
X	X	FT	macromolecular carrier gp. attached"
X	X	FT	
X	X	FT	/note= "optionally has a carboxyl, amido, hydrophobic
X	X	FT	or macromolecular carrier gp. attached"

WO959615-A1.
XX
25 NOV-1999.
XX
20-MAY-1999; 99WO-US11219.
XX
20-MAY-1998; 98US-0082279.
XX
(TRIM-) TRIMERIS INC.
XX
Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
WPI; 2000-136792/12.
A new hybrid polypeptide with enhanced pharmacokinetic properties
comprises enhancer sequence -
Disclosure; Page 31; 124pp; English.
The invention relates to hybrid polypeptides comprising enhancer peptide
sequenced linked to core polypeptides. The enhancer polypeptides are
derived from various retroviral envelope (gp41) protein sequences,
especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
pharmacokinetic properties such as increasing the half-life of any core
polypeptide that they are linked to. The core polypeptides are any
polypeptide that may be introduced into a living system and that can
function as a pharmacologically useful peptide for the treatment or
prevention of a disease. The core polypeptides are bioactive peptides
selected from growth factor, cytokine, differentiation factor,
interleukin, interferon, colony stimulating factor, hormone or angiogenic
factor. The peptides of the invention can be used for inhibiting viral
infection and can be used in anti-viral and anti-fusogenic treatments.
Sequences y8651-y9055 represent core polypeptide fragments that can be
used in the invention. Some sequences among those indicated also comprise
antiviral activity of this peptide is not stated in the
specification.
XX
WO9428920-A.
XX
22-DEC-1994.
PD
XX
07-JUN-1994; 94WO-US05739.
XX
07-JUN-1993; 93US-0073028.
XX
(YUDU-) UNIV DUKE.
PA
Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;
PI
Petway SR, Wild CR;
XX
WPI; 1995-036105/05.
XX
Computer search generated synthetic peptides - are inhibitors of
HIV transmission
PT
PT
HIV transmission
XX
Claim 14; Page 138; 182pp; English.
PS
R64591-623 are peptide derivatives of a 37 mer RF-1 peptide derived
from respiratory syncytial virus (RSV) (R64590) which have been
truncated at the amino terminus. The peptides are DP-178 like
peptides. DP-178 corresponds to amino acids 638 to 673 of the HIV-1
isolate LAI transmembrane protein gp41. It forms a putative alpha
helix at the C-terminal end of the gp41 ectodomain, and complexes
with DP-107 (corresponds to amino acids 558-595) which contains a
leucine zipper motif. The peptides complex via non-covalent
protein-protein interactions. The peptide derivatives were
identified by a computer assisted peptide sequence search. The
antiviral activity of this peptide is not stated in the
specification.
XX
PS
R64591-623 are peptide derivatives of a 37 mer RF-1 peptide derived
from respiratory syncytial virus (RSV) (R64590) which have been
truncated at the amino terminus. The peptides are DP-178 like
peptides. DP-178 corresponds to amino acids 638 to 673 of the HIV-1
isolate LAI transmembrane protein gp41. It forms a putative alpha
helix at the C-terminal end of the gp41 ectodomain, and complexes
with DP-107 (corresponds to amino acids 558-595) which contains a
leucine zipper motif. The peptides complex via non-covalent
protein-protein interactions. The peptide derivatives were
identified by a computer assisted peptide sequence search. The
antiviral activity of this peptide is not stated in the
specification.
XX

SO Sequence 20 AA;

Query Match 55.8%; Score 24; DB 16; Length 20;
Best Local Similarity 66.7%; Pred. No. 1.1e-02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 K1FGSLAFL 9
Db 5 kingslafi 13

RESULT 25

ID Y82864 standard; peptide; 9 AA.

XX Y82864;

XX 19-JUN-2000 (first entry)

XX Uroplakin tumour associated antigen (TAA).

DE Tumour associated antigen peptide; TAA: cancer: carcinoma;
KW treatment; prevention; cure; anti-tumour vaccine; metastases;
KW breast; bladder; prostate; pancreas; ovary; thyroid; colon;
KW stomach; carcinoma; MHC Class I; HLA-A2; human;
KW Major Histocompatibility Complex; uroplakin;
KW prostate specific antigen; prostate specific membrane antigen;
KW prostate acid phosphatase; mucin; lactadherin; PSA; PSMA; PAP; CRIPTO-1.
KW teratocarcinoma derived growth factor; PSA; PSMA; PAP; CRIPTO-1.

OS Homo sapiens.

XX WO200006733-A1.

XX 10-FEB-2000.

XX PF 29-JUL-1999;

XX PR 30-JUL-1998; 981L-012568.

XX PA (YEDA) YEDA RES & DEV CO LTD.
PA (BIOT) BIO-TECHNOLOGY GEN CORP.

XX PI Eisenbach L, Carmon L, Tirosh B, Bar-haim E, Paz A, Fridkin M;
PI Fitzner-atlas C;

XX WPI: 2000-205463/18.

XX Tumor associated antigen peptides, especially derived from uroplakin, useful as vaccines to prevent or cure cancers including breast, bladder, prostate, pancreas, ovary, thyroid, colon and stomach.

XX Claim 4; Page 104; 113pp; English.

XX Tumour associated antigen peptides (TAA) may be used for the treatment, prevention and cure of cancer or cancer metastases. The cancer may be breast, bladder, prostate, pancreas, ovary, thyroid, colon, stomach, head or neck cancer or a carcinoma. The tumour associated antigens are presentable to the immune system by HLA-A2 molecules and are generally between 8 to 10 amino acids in length. The amino acids located at positions 2 and 9 of the tumour associated antigens are the anchor residues which participate in the binding to MHC class I molecules, more specifically HLA-A2. More tumour associated antigens are described in GENSEQ records Y82806-Y82882. Those tumour associated antigens described in records Y82806-Y82824 and Y82855-Y82869 are derived from Uroplakin I, such as Uroplakin Ia, Uroplakin Ia, Uroplakin III and Uroplakin Iib. Those described in records Y82825-Y82829 are derived from prostate specific antigen (PSA). Those described in records Y82830-Y82835 are derived from prostate specific membrane antigen (PSMA). Those described in records Y82836-Y82839 are derived from prostate acid phosphatase (PAP). Those described in records Y82840-Y82846 are derived from Lactadherin (BA-46). Those described in records Y82847-Y82854 are derived from Mucin and those described in records Y82871-Y82882 are derived from Teratocarcinoma derived growth factor (CRIPTO-1).

CC CC are derived from Mucin and those described in records Y82871-Y82882.
CC CC are derived from Teratocarcinoma derived growth factor (CRIPTO-1).

XX SQ Sequence 9 AA;

Query Match 53.5%; Score 23; DB 21; Length 9;
Best Local Similarity 71.1%; Pred. No. 2.1e-05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 1FGSLAFL 8
| ||| |
Db 1 ilgslpf 7

Search completed: November 14, 2000, 11:57:26
Job time: 33 sec

